

STIC-Biotech/ChemLib

99351

CRF

From: Chan, Christina
S nt: Monday, July 21, 2003 3:21 PM
To: Davis, Minh-Tam; STIC-Biotech/ChemLib
Subject: RE: Rush search request for 09/878454

Please ~~rush~~ Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644
308-3973
CM-1, 9B19

-----Original Message-----

From: Davis, Minh-Tam
Sent: Monday, July 21, 2003 3:21 PM
To: Chan, Christina
Subject: Rush search request for 09/878454

Please search in commercial database, PGPUB and issued patent files:
SEQ ID NO:2, wherein one amino acid of the amino acids at positions 160-173 is mutated. That is a sequence with
Xaa at any one position of amino acids 160-173 of SEQ ID NO:2.

Thank you.

MINH-TAM DAVIS
ART UNIT 1642 ROOM 8A01 MB 8E12
305-2008

Seq 2 AA 191

mej

party date?

RECEIVED
JUL 21 2003
6/20/03

Searcher: P. Schreiber
Phone: 308-4392
Location: CM 16A03
Date Picked Up: _____
Searcher Prep/Review: 15
Clerical: _____
Online time: 34

Completed
7/24

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: 1
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: CompuLink
WWW/Internet: _____
Other (specify): _____

GenCore version 5.1.6
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OK protein - protein search, using sw model

Run on: July 24, 2003, 12:55:51 ; Search time 85 Seconds

(Without alignments)
356.668 Million cell updates/sec

Title: SEQ2_MOD

Perfect score: 905

Sequence: 1 MGSGSRSLKELAEYQDLT.....XXQHVISRSPDPASSFKIVL 191

Scoring table: BLOSUM62JDX

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_19Jun03:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	901	99.6	191	AAW51215	Amino acid sequenc
2	893	98.7	191	AAW64199	Human interferon r
3	876	96.8	191	AAW62287	Human protein phos
4	352	38.9	172	AAU87324	Novel central nerv
5	352	38.9	184	AAW43562	Human polypeptide
6	350	38.7	185	AAW64418	Amino acid sequenc
7	342.5	37.8	201	ABR4480	Human intracellular
8	326	36.0	173	ABB96054	Human testicular a
9	326	36.0	173	AAU87612	Novel central nerv

10	326	36.0	173	22	AAW95362	Human reproductive
11	326	36.0	173	22	AAW43637	Human polypeptide
12	326	36.0	173	22	AAU19952	Novel human calcit
13	324	35.8	187	22	AAE09736	Human kinase inter
14	324	35.8	187	22	ABG30437	Human protein sequ
15	318.5	35.2	206	22	ABW64325	Drosophila melanog
16	279.5	30.9	182	24	ABW99404	Amino acid sequenc
17	278.5	30.8	220	24	ABG30435	Human protein sequ
18	223.5	24.7	169	23	ABP41194	Human ovarian anti
19	217	24.0	120	20	AAI1976	Human 5' EST secre
20	194	21.4	175	21	AAI21178	Zea mays protein f
21	194	21.4	210	21	AAI21177	Zea mays protein f
22	190	21.0	175	21	AAI21176	Arabidopsis thalia
23	190	21.0	175	23	ABW92357	Herbicidally activ
24	188	20.8	175	23	AAI21175	Calcineurin regula
25	184.5	20.4	175	20	AAI21174	Arabidopsis thalia
26	181	20.0	169	21	AAI21173	Zea mays protein f
27	180	19.9	169	21	AAI21172	Arabidopsis thalia
28	179	19.8	169	21	AAI21171	Human CBP1 protein
29	175.5	19.4	189	22	ABW8936	Drosophila melanog
30	166.5	18.4	187	22	ABW8935	Human calcineurin
31	165.5	18.3	170	19	AAW64200	Human calcineurin
32	165.5	18.3	170	21	AAW64200	Human calcineurin
33	164.5	18.2	110	23	ABG30435	Human HCNB protein
34	162.5	18.0	195	24	ABG74662	Human protein sequ
35	159.5	17.6	187	22	ABW67063	Murine Ca2+-bindin
36	157.5	17.4	195	24	ABG74661	Drosophila melanog
37	157	17.3	214	20	AAI31625	Human Ca2+-binding
38	157	17.3	257	22	AAI31625	Human calcineurin
39	153.5	17.0	226	21	AAI31625	Human colon cancer
40	152.5	16.9	226	21	AAI31625	Arabidopsis thalia
41	152.5	16.9	226	21	AAI31625	Arabidopsis thalia
42	152	16.8	226	21	AAI31625	Arabidopsis thalia
43	152	16.8	170	21	AAI31625	Human CBP1 protein
44	152	16.8	173	22	AAI31625	Calcineurin B subu
45	152	16.8	187	22	AAU87327	Amino acid sequenc
						Novel central nerv

ALIGNMENTS

RESULT 1	AAW51215	standard; Protein: 191 AA.
ID	AAW51215	
XX	AAW51215:	
AC	21-AUG-1998	(first entry)
DT		
DE		Amino acid sequence of the calcium-integrin binding protein.
XX		
KW		Human calcium-integrin binding protein; CIB; Integrin alpha IIB;
KW		Cytoplasmic domain; platelet; alpha IIB-beta-3; fibrinogen receptor;
KW		Inhibition; blood coagulation; vascular disorder.
XX		
OS		Homo sapiens.
XX		
FH	Key	Location/Qualifiers
FT	Region	116..128
FT	Region	/note="EF-hand motif"
FT	Region	160..173
FT	Region	/note="EF-hand motif"
PN		
PN	W09814471-A1.	
XX		
PD	09-APR-1998.	
XX		
PF	24-SEP-1997;	97WO-US16828.
XX		
PR	02-OCT-1996;	96US-0720625.
XX		
PA	(UYN-C) UNIV NORTH CAROLINA.	
XX		

5

DR	WP1: 1998-414096/35.
DR	N-PsDB: AAY44272.
PT	New isolated interferon receptor binding proteins - used to develop
PT	products for modulating sensitivity to interferon, e.g. in the
PT	treatment of tumours or for prolonging graft survival
PS	Claim 1; Page 34; 6app; English.
XX	
CC	This is a novel human protein, designated interferon receptor
CC	binding protein 1 (IRB1), which interacts with the intracytoplasmic
CC	(IC) domain of the IFNAR1 chain of the interferon type 1 (IFN-alpha,
CC	beta or omega) receptor. IRB1 is a new member of the calcineurin
CC	and caltactrin family of calcium-regulated proteins (see also
CC	AAM64200). It is induced very rapidly and transiently following IFN
CC	treatment of human cells. It was identified in a two-hybrid
CC	screening for proteins interacting with the IFNAR1-IC domain;
CC	another protein, IRIB4 (see AAM64202), was similarly identified. A
CC	cDNA clone (see AAY44272) encoding IRB1, host cells and expression
CC	vectors are claimed. DNA encoding IRB1 and IRIB4 can be used in
CC	cancer therapy where the increased cellular response to IFN would
CC	result in a decrease in malignant cell growth and an enhanced
CC	response to exogenous IFN therapy. Antisense IRB1 or IRIB4
CC	nucleic acids can be used for prolonging tissue or organ graft
CC	survival in patients as the rejection of these grafts in the host
CC	is mediated by the histocompatibility antigens (MHC class I) whose
CC	synthesis depends on the IFN stimulus. The products can also be
CC	used in detection and diagnosis.
SQ	Sequence 191 AA;
	Query Match 98.7%; Score 893; DB 19; Length 191;
	Best Local Similarity 91.6%; Pred. No. 3.7e-78;
	Matches 175; Conservative 15; Mismatches 1; Indels 0; Gaps 0
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DB	1 MGSGSRSLKELAEVQDLFTLKOEILLAAHRRFCELLPOEORSSESSLRRAVPFEQLS 60
OY	61 LPELKANFERKERICEVFSTSPAKDLSFEDEFLDLVSVDTPPIKSHYAFRIPFPDD 120
DB	61 LPELKANFERKERICEVFSTSPAKDLSFEDEFLDLVSVDTPPIKSHYAFRIFFDD 120
OY	121 GTLNREDLSRLVNCITGEGEDTRLSASEMKOLINDLEEXXXXXXXXQXHVIRS 180
DB	121 GTLNREDSRLVNCITGEGEDTRLSASEMKOLIDYILLESPIIDRDGTINLSFQIVIRS 180
OY	181 PDFASSFRIYL 191
DB	181 PDFASSFRIYL 191
RESULT 3	
AAW62287	
AAW62287	standard; Protein: 191 AA.
XX	
AC	AAW62287;
XX	
DT	24-SEP-1998 (first entry)
XX	
DE	Human protein phosphatase regulatory subunit.
XX	
KW	Human; protein phosphatase regulatory subunit; HCNB; diagnosis;
XX	immunosuppression; neurodegeneration; inflammation; cancer.
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	Misc-difference 44
FT	/label= unknown
FT	/note= "encoded by ASG"
FT	Misc-difference 45
FT	/label= unknown

FT XX /note= "encoded by TGN"
 PN XX MO9826056-A1.
 PD XX 18-JUN-1998.
 XX XX
 PF XX 25-NOV-1997; 97WO-US21603.
 XX XX
 PR XX 12-DEC-1996; 96US-0764563.
 XX XX
 PA (IMCY-) INCYTE PHARM INC.
 XX XX
 PI Goli SK, Hillman JL;
 XX XX
 DR WPI: 1998-348518/30.
 XX XX
 PT New protein phosphatase regulatory sub-unit - useful for diagnosis,
 PT prevention and treatment of immuno-suppression, neuro-degeneration,
 PT inflammation and cancer
 XX XX
 PS Claim 1; Fig 1; 65pp; English.
 XX XX
 CC The present sequence is a pure human protein phosphatase regulatory
 CC subunit (HCNB). Host cells, comprising a vector containing DNA encoding
 CC HCNB, are used to produce recombinant HCNB which is used to treat or
 CC prevent immunosuppression or neurological diseases (especially parasitic,
 CC bacterial or viral infections, including AIDS; the effects of radio- or
 CC chemo-therapy and Alzheimer's disease). Antagonists which bind
 CC specifically to HCNB and modulate its activity are used to treat
 CC inflammation, cancer, or immunological disorders and allograft rejection
 CC (especially anemia, asthma, systemic lupus erythematosus, myasthenia
 CC gravis, diabetes, thyroiditis, ulcerative colitis, osteoporosis and
 CC arthritis). Complements of the DNA encoding HCNB are useful as probes
 CC and primers for detecting the DNA encoding HCNB by hybridisation or
 CC amplification assays, while Ab can be used to detect HCNB by immunoassay,
 CC particularly for diagnosis of the specified disorders, including early
 CC diagnosis of cancers. The probes can also be used to map the
 CC screening and for purifying native HCNB. Therapeutic agents are
 CC administered orally, intravenously, intramuscularly, topically or
 CC rectally, normally at 0.1-105 mg g.
 CC XX
 SQ Sequence 191 AA;
 Query Match 96.8%; Score 876; DB 19; Length 191;
 Best Local Similarity 91.6%; Pred. No. 1,7e-76;
 Matches 175; Conservative 14; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MGSGSRLSKELAEYQDLFLTKQETLLAHRFCCLPQEOETVSSLRQVPEFOIIS 60
 DB 1 MGSSSRSLKELAEYQDLFLTKQETLLAHRFCCLPQEOEXXSSLRQVPEFOIIS 60
 QY 61 LPELKAMPKERICRSTSPAKDSLSFEDFLDLVSFSDTATPDIKSHYAFRIFPD 120
 DB 61 LPELKAMPKERICRSTSPAKDSLSFEDFLDLVSFSDTATPDIKSHYAFRIFPD 120
 QY 121 GLNREDLSRLNCLTGEGETRLSSEKQKIDNILEXXXKXKXKXQXHYISS 180
 DB 121 GLNREDLSRLNCLTGEGETRLSSEKQKIDNILESDIDRQGTINLSEFOHYISS 180
 QY 181 PDFASSFKIVL 191
 DB 181 PDFASSFKIVL 191
 RESULT 4
 ID AA087324 standard; Protein; 172 AA.
 AC AA087324;
 DT 05-JUN-2002 (first entry)

DE Novel central nervous system protein #234.
 XX
 KW Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
 KW hyperproliferative disorder; neoplasm; cardiovascular disorder;
 KW cardiac arrest; cerebrovascular disorder; ischemia; anglogenesis;
 KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
 KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;
 KW adenocarcinoma; reproductive system disorder; testicular feminisation;
 KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;
 KW respiratory disorder; renal disorder; kidney failure; blood disorder;
 KW myocardial infarction; wound healing; cell proliferation; skin aging;
 KW food additive; food preservative; gene therapy.
 XX
 OS Homo sapiens.
 XX
 XX MO20015318-A2.
 PD 02-AUG-2001.
 XX
 XX 17-JAN-2001; 2001WO-US01332.
 PF
 XX
 PR 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180628.
 PR 24-FEB-2000; 2000US-0184664.
 PR 02-MAR-2000; 2000US-0186350.
 PR 16-MAR-2000; 2000US-0189874.
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 PR 18-APR-2000; 2000US-0198123.
 PR 19-MAY-2000; 2000US-0205515.
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PR 01-DEC-2000; 2000US-0250391.

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PR 08-DEC-2000; 2000US-0251899.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
PI WPI; 2001-581633/65.
DR N-PSDB; ABK43654.
XX
PT New isolated nucleic acid encoding a protein for diagnosing,
PT Preventing, treating or ameliorating medical conditions and used as
XX food additives or preservatives -
XX
PS Claim 9; SEQ ID NO 842; 837pp; English.
XX
CC The invention describes an isolated nucleic acid molecule (I) encoding a
CC novel central nervous system protein. (I) and polypeptides (II) encoded
CC by (I), are used to treat a medical conditions and in diagnosis of a
CC pathological condition. Disorders which are diagnosed or treated include
CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischemia,
CC angiogenesis, nervous system disorders e.g. Alzheimer's disease and
CC amyotrophic lateral sclerosis, infections caused by bacteria, viruses
CC e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders
CC e.g. corneal infection, gastrointestinal disorders e.g. dysphagia,
CC adenocarcinomas and irritable bowel syndrome, reproductive system
CC disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes
CC and pituitary dwarfism, cancers and disorders at the cellular level e.g.
CC leukaemia, disorders involving neovascularisation e.g. malignancies,
CC respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g.
CC acute kidney failure and blood related disorders e.g. myocardial
CC infarction. The polypeptides can also be used to aid wound healing and
CC epithelial cell proliferation, to prevent skin aging due to sunburn, to
CC maintain organs before transplantation, for supporting cell culture of
CC primary tissues, to regenerate tissues and in chemotaxis. The
CC polypeptides can also be used as a food additive or preservative to
CC increase or decrease storage capabilities, fat content, lipid, protein,
Query Match 38.9%; Score 352; DB 22; Length 172;
Best Local Similarity 40.1%; Pred. No. 1.6e-25;
Matches 71; Conservative 47; Mismatches 49; Indels 10; Gaps 3;
QY 13 LAEYODLPLTRKOEILAHRRFCELLPQORVYESSLRQVPEOLISPELKANPFKER 72
DB 1 LEEYQALTLTRNEILCHIDTLFLKCPKRYKEATL----TMDYSSLPALRVNPFRRD 56
QY 73 ICRVFTSPAKDLSFEDELDFLLSVFSDATPDIKSHVAFRTFDDDDGTLNEDLSRLV 132
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RESULT 5
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XX
XX AAM43562;
AC
XX
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DT 22-OCT-2001 (first entry)


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PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
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XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI: 2001-488781/53.
XX
XX N-PSDB; AAI63868.
XX
XX New isolated nucleic acids and polypeptides, useful for diagnosing,
XX treating and/or preventing human diseases and disorders -
XX
XX Claim 11: SEQ ID NO 240; 664pp + Sequence Listing; English.
XX
XX The invention relates to human polynucleotides (AAI63803-AAI64012) and
XX the encoded proteins (AAI634497-AAI63660) useful for preventing, treating
XX or ameliorating medical conditions e.g. by protein or gene therapy. The
XX genes were isolated from a range of human tissues disclosed in the
XX specification. The nucleic acids, proteins, antibodies and (ant)agonists
XX are useful in the diagnosis, treatment and prevention of: (a) cancer,
XX e.g. breast and ovarian cancer and other cancers of the adrenal gland,
XX bone, bone marrow, breast, gastrointestinal tract, liver, lung, or
XX urogenital; (b) immune disorders e.g. Addison's disease, allergies,
XX autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
XX Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
XX colitis; (c) cardiovascular disorders such as myocardial ischaemias;
XX (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
XX epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
XX and parasitic infections.
XX Note: The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 184 AA:
XX
XX Query Match 38.9%; Score 352; DB 22; Length 184;
XX Best Local Similarity 40.1%; Pred. No. 1.8e-25;
XX Matches 71; Conservative 47; Mismatches 49; Indels 10; Gaps 3;
XX
XX 13 LAEYQDLEFTRKQELLAHRRFCELLPOEQRTVESSLRQVPEFQILSLPELKANPFKER 72
XX 13 LEEYQALTEFTRNEIICIHDTFLKCPGKYKKEATL---TMDQVSSLPALVNPFRDR 68
XX
XX 73 ICFVFTSPAKDLSFEDFLDLVSFSDTATPDIKSHYAFRIEDDDGTLNEDLSRLV 132
XX 69 ICFVFS---HKGMSFSEFVGLMASVSEQACPSLKEIYAFRIYDFNENGFIDEDLQRII 125
XX
XX 133 NCTGTGEGDTRLASSEMKQILDNIIEEXXXXXXXXOVIVSRSPPEASFSFI 189
XX 126 IIRLNSDD---MSEDLMDLTNHNVLSESLDNDNMLSFSEFHHAAKSPDEWMSFRI 179
XX
XX RESULT 6
XX AAB64418
XX ID AAB64418 standard; protein; 185 AA.
XX
XX AAB64418:
XX
XX 22-MAR-2001 (first entry)
XX
XX Amino acid sequence of human intracellular signalling molecule INTRA50.
XX DE Human; intracellular signalling molecule; INTRA; immunosuppressive;
XX KW cytosolic; neuroprotective; neurotropic; antiarteriosclerotic; cancer;
XX KM antiinflammatory; anti-HIV; neuroleptic; antibacterial; antifungal;

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KW antiviral; antiparasitic; antihelminthic; antiparkinsonian; AIDS;
KW cell proliferative disorder; arteriosclerosis autoimmune; epilepsy;
KW inflammatory disorder; Addison's disease; gastrointestinal disorder;
KW neurological disorder; Parkinson's disease; Creutzfeldt-Jakob disease;
KW mental disorder; schizophrenia; anxiety.
XX
XX Homo sapiens.
XX
XX W0200077040-A2.
XX
XX 21-DEC-2000.
XX
XX 16-JUN-2000; 2000WO-US16636.
XX
XX 16-JUN-1999; 99US-0139566.
XX 17-AUG-1999; 99US-0149640.
XX 09-NOV-1999; 99US-0164417.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Yue H, Tang YT, Hillman JL, Lai P, Bandman O, Baughn MR;
XX PI Azimzai Y, Yang J, Reddy R, Lu DM;
XX
XX WPI: 2001-025334/03.
XX
XX N-PSDB; AAF32687.
XX
XX New human intracellular signalling molecules, useful for the diagnosis,
XX prevention and treatment of cell proliferative, autoimmune,
XX inflammatory, neurological, gastrointestinal, reproductive and
XX developmental disorders -
XX
XX Claim 5; Page 158-159; 192pp; English.
XX
XX Sequences AAF32638 - AAF32689 represent cDNA encoding human
XX intracellular signalling molecules INTRA1 - INTRA52, represented in
XX AAB64369 - AAB64420. Modulators of the intracellular signalling molecules
XX of the invention exhibit immunosuppressive, cytosolic, neuroprotective;
XX neurotropic; antiarteriosclerotic; antiinflammatory; anti-HIV;
XX neuroleptic; antibacterial; antifungal; antiviral; antiparasitic;
XX antihelminthic; and antiparkinsonian activity. INTRA polypeptides their
XX agonists and antagonists are useful for the treatment of a condition
XX associated with decreased or increased expression of functional INTRA
XX disorders associated with abnormal INTRA expression or activity include
XX cell proliferative disorders e.g. arteriosclerosis and cancers;
XX autoimmune or inflammatory disorders e.g. Addison's disease and acquired
XX immunodeficiency syndrome (AIDS); viral, bacterial, fungal, parasitic,
XX protozoal and helminthic infections; gastrointestinal disorders e.g.
XX dysphagia and irritable bowel syndrome; neurological disorders e.g.
XX epilepsy and Parkinson's disease; prion diseases e.g. Creutzfeldt-Jakob
XX disease and mental disorders e.g. anxiety, schizophrenia and Tourette's
XX disorder. Antibodies immuno specific for the INTRA proteins may also be
XX useful in the diagnosis of the above disorders.
XX
XX Sequence 185 AA:
XX
XX Query Match 38.7%; Score 350; DB 22; Length 185;
XX Best Local Similarity 40.2%; Pred. No. 2.8e-25;
XX Matches 72; Conservative 46; Mismatches 51; Indels 10; Gaps 3;
XX
XX 11 ELAEYQDLEFTRKQELLAHRRFCELLPOEQRTVESSLRQVPEFQILSLPELKANPFK 70
XX 12 EDEYQALTEFTRNEIICIHDTFLKCPGKYKKEATL---TMDQVSSLPALVNPFR 67
XX
XX 71 ERICRVFTSPAKDLSFEDFLDLVSFSDTATPDIKSHYAFRIEDDDGTLNEDLSRLV 130
XX 68 DRICRVFS---HKGMSFSEFVGLMASVSEQACPSLKEIYAFRIYDFNENGFIDEDLQRI 124
XX
XX 131 LVNCLTGTGEGDTRLASSEMKQILDNIIEEXXXXXXXXOVIVSRSPPEASFSFI 189
XX 125 IIRLNSDD---MSEDLMDLTNHNVLSESLDNDNMLSFSEFHHAAKSPDEWMSFRI 180
XX
XX RESULT 7

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ABR48480
ID ABR48480 standard; Protein; 201 AA.
XX
AC ABR48480;
XX
DT 13-JUN-2003 (first entry)
XX
DE Human Intracellular signalling protein.
XX
KW Human; GENSET; therapeutic; therapy.
XX
OS Homo sapiens.
XX
PN MO200294864-A2.
XX
PD 28-NOV-2002.
XX
PF 06-AUG-2001; 2001MO-IB01715.
XX
PR 25-MAY-2001; 2001US-293574P.
XX
PR 15-JUN-2001; 2001US-298698P.
XX
PR 29-JUN-2001; 2001US-302277P.
XX
PR 13-JUL-2001; 2001US-305456P.
XX
PA (GENSET ) GENSET.
XX
PI Benjamin S, Tanaka H;
XX
DR WPI; 2003-129412/12.
XX
DR N-PDB; ACCS1087.
XX
PT New GENSET polynucleotides and polypeptides, useful for preparing a
composition for treating GENSET-related disorders and as reagents in
assays to quantitatively determined levels of GENSET expression in
biological samples -
XX
PS Claim 2; Page 449; 505pp; English.
XX
XX
XX
The present invention relates to novel human GENSET coding sequences
CC (ACC51060-ACC51115) and proteins (ABR48453-ABR48508). The GENSET
CC sequences are useful for preparing a composition for treating
CC GENSET-related disorders. They can also be used as markers for tissues in
CC which the corresponding protein is preferentially expressed, as molecular
CC weight markers on Southern gels, as chromosome markers or tags to
CC identify chromosomes, and as reagents in assays to quantitatively
determined levels of GENSET expression in biological samples.
XX
SQ Sequence 201 AA.
Query Match 37.8%; Score 342.5; DB 24; Length 201;
Best Local Similarity 38.6%; Pred. No. 1.8e-24;
Matches 73; Conservative 49; Mismatches 54; Indels 13; Gaps 4
QY 1 MGSSSRSLKELLAETQDITFLTKOELLAHRRFCELLPQEQRTVESSLRAQVPFEQLIS 60
DB 21 MNGVDTSLLCDL---QALTEFLTRREILICIHDTFLFKLCPPGKYKEATL---TMDQVS 73
QY 61 LPELKANFKKEIKCVESFSPAKDSLSPEDFDLSVSDTATPOIKSHYARIDEFDD 120
DB 74 LPALRVNFFRDRIKCVFS--HKGFSEFEDYGVMSAVSEQPCSLKTEYARIRDFNEN 130
QY 121 GTLNREDLSRYNCLTGEGEDTRLASASEMKOLINDIIEXXXXXXXHXHVIHS 180
DB 131 GFIDBEDLQRITRLRLNSD---MSEDLLMDLTNRHVLSESDLNDNMLSFSEFHAMAKS 187
QY 181 PDFASSFKI 189
DB 188 PDFMNSPRI 196

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XX	AC	AB96054;
XX	DT	21-JUN-2002 (first entry)
XX	DE	Human testicular antigen SEQ ID NO: 1438.
XX	KM	Human; testicular antigen; testes; cancer; metastasis; immune disorder
XX	KW	reproductive system disorder; urinary system disorder; gene therapy;
XX	KW	cardiovascular disorder; respiratory disorder; neurological disorder;
XX	OS	gastrointestinal disease; infection; cytostatic.
XX	PN	Homo sapiens.
XX	PD	WO200155317-A2.
XX	PD	02-AUG-2001.
XX	PF	17-JAN-2001; 2001WO-US01329.
XX	PR	31-JAN-2000; 2000US-0179065.
XX	PR	04-FEB-2000; 2000US-0180628.
XX	PR	24-FEB-2000; 2000US-0184664.
XX	PR	02-MAR-2000; 2000US-0186350.
XX	PR	16-MAR-2000; 2000US-0189874.
XX	PR	17-MAR-2000; 2000US-0190076.
XX	PR	18-APR-2000; 2000US-0198123.
XX	PR	19-MAY-2000; 2000US-0205515.
XX	PR	07-JUN-2000; 2000US-0209467.
XX	PR	28-JUN-2000; 2000US-0214886.
XX	PR	30-JUN-2000; 2000US-0215135.
XX	PR	07-JUL-2000; 2000US-0216647.
XX	PR	07-JUL-2000; 2000US-0216880.
XX	PR	11-JUL-2000; 2000US-0217487.
XX	PR	14-JUL-2000; 2000US-0217496.
XX	PR	26-JUL-2000; 2000US-0218290.
XX	PR	26-JUL-2000; 2000US-0220961.
XX	PR	14-AUG-2000; 2000US-0224518.
XX	PR	14-AUG-2000; 2000US-0225219.
XX	PR	14-AUG-2000; 2000US-0225219.
XX	PR	14-AUG-2000; 2000US-0225219.
XX	PR	14-AUG-2000; 2000US-0225219.
XX	PR	14-AUG-2000; 2000US-0225266.
XX	PR	14-AUG-2000; 2000US-0225267.
XX	PR	14-AUG-2000; 2000US-0225267.
XX	PR	14-AUG-2000; 2000US-0225270.
XX	PR	14-AUG-2000; 2000US-0225447.
XX	PR	14-AUG-2000; 2000US-0225757.
XX	PR	14-AUG-2000; 2000US-0225758.
XX	PR	14-AUG-2000; 2000US-0225759.
XX	PR	18-AUG-2000; 2000US-0226279.
XX	PR	22-AUG-2000; 2000US-0226681.
XX	PR	22-AUG-2000; 2000US-0226866.
XX	PR	22-AUG-2000; 2000US-0227182.
XX	PR	23-AUG-2000; 2000US-0227009.
XX	PR	30-AUG-2000; 2000US-0228924.
XX	PR	01-SEP-2000; 2000US-0229287.
XX	PR	01-SEP-2000; 2000US-0229343.
XX	PR	01-SEP-2000; 2000US-0229344.
XX	PR	01-SEP-2000; 2000US-0229345.
XX	PR	05-SEP-2000; 2000US-0229509.
XX	PR	05-SEP-2000; 2000US-0229513.
XX	PR	06-SEP-2000; 2000US-0230437.
XX	PR	06-SEP-2000; 2000US-0230438.
XX	PR	08-SEP-2000; 2000US-0231242.
XX	PR	08-SEP-2000; 2000US-0231243.
XX	PR	08-SEP-2000; 2000US-0231244.
XX	PR	08-SEP-2000; 2000US-0231413.
XX	PR	08-SEP-2000; 2000US-0231414.
XX	PR	08-SEP-2000; 2000US-0232080.
XX	PR	08-SEP-2000; 2000US-0232081.
XX	PR	12-SEP-2000; 2000US-0231968.
XX	PR	14-SEP-2000; 2000US-0232397.

XX 02-AUG-2001.
PD
XX
PF 17-JAN-2001; 2001WO-US01332.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0186874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226688.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229349.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
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PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
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PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
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PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
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PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.

PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241836.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249284.
PR 17-NOV-2000; 2000US-0249285.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 11-DEC-2000; 2000US-0251990.
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.
PA
XX
PI Rosen CA, Barash SC, Ruben SM;
XX

DR MPI: 2001-581633/65.
PR N-PSDB: ABR43942.
XX
PR New isolated nucleic acid encoding a protein for diagnosing.
PR Preventing, treating or ameliorating medical conditions and used as
PR food additives or preservatives -
XX
PS Claim 9; SEQ ID No. 1130; 837pp; English.
XX
CC The invention describes an isolated nucleic acid molecule (I) encoding a
CC novel central nervous system protein. (I) and polypeptides (II) encoded
CC by (I), are used to treat a medical condition and in diagnosis of a
CC pathological condition. Disorders which are diagnosed or treated include
CC autoimmune diseases e.g. Rheumatoid arthritis, hyperproliferative
CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
CC angioneurosis, nervous system disorders e.g. Alzheimer's disease and
CC amyotrophic lateral sclerosis, infections caused by bacteria, viruses
CC e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders
CC e.g. corneal infection, gastrointestinal disorders e.g. dysphagia,
CC adenocarcinomas and irritable bowel syndrome, reproductive system
CC and pituitary dwarfism, cancers and disorders at the cellular level e.g.
CC leukaemia, disorders involving neovascularisation e.g. malignancies,
CC respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g.
CC acute kidney failure and blood related disorders e.g. myocardial
CC infarction. The polypeptides can also be used to aid wound healing and
CC epithelial cell proliferation, to prevent skin aging due to sunburn, to
CC maintain organs before transplantation, for supporting cell culture of
CC primary tissues, to regenerate tissues and in chemotaxis. The
CC polypeptides can also be used as a food additive or preservative to
CC increase or decrease storage capabilities, fat content, lipid, protein,
CC
Query Match 36.0%; Score 326; DB 22; Length 173;
Best Local Similarity 38.9%; Pred. No. 5.4e-23;
Matches 68; Conservative 46; Mismatches 51; Indels 10; Gaps 3;
QY 13 LAEYODLFLTKOELLARHRCCELLPQORVYESSLRACVPEQILSLPELKANPKER 72
DB 1 LEEYQALFLTRNEICLHDFTFLKCPKRYKKEATL---TMDQVSSLPALRVNPFDR 56
QY 73 ICRVSTSPAKDLSFEDFLDLSVSPDTPDIKSHVAFRIFFPDGDTLRNEDSLRY 132
DB 57 ICRVTS---HKGMFSEEDVLGMASVSEACPSLKEIVAFRIYDENENFIDEEDQRII 113
QY 133 NCLTGEDEPTLSASEMQLIDNILEXXXXXXXHXHVISRSPDFASSF 187
DB 114 LRLNSDD--MSEDLMDLTNHVLSXSDLDNMLSEFPHMAKSKDFMTPF 165
RESULT 10
AAM95362
ID AAM95362 standard; Protein; 173 AA.
XX
AC AAM95362;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human reproductive system related antigen SEQ ID NO: 4020.
XX
KM Human; reproductive system related antigen; reproductive system disorder;
XX cancer; gene therapy.
OS Homo sapiens.
XX
PM WO200155320-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01339.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.

PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
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PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
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PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226688.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229349.
PR 05-SEP-2000; 2000US-0229509.
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PR 08-SEP-2000; 2000US-0231242.
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PR 08-SEP-2000; 2000US-0231244.
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PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
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PR 02-OCT-2000; 2000US-0237038.

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PR	05-JAN-2001	2001US-0259678
PA	(HUMA-)	HUMAN GENOME SCI INC.
PI	Rosen CA,	Barash SC, Ruben SM;
XX	WPI:	2001-465570/50.
DR	N-PSDB:	AAI01332.
XX		
PT	Isolated nucleic acid molecule encoding a reproductive system antigen	
XX	is used in preventing, treating or ameliorating a medical condition	
XX	Claim 11; SEQ ID NO 4020; 1297bp + Sequence Listing; English.	

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PR	08-NOV-2000	2000US-0244641	
PR	08-NOV-2000	2000US-0244641	

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;
WPI: 2001-465568/50.
DR N-PDB; AAS31637.

Isolated nucleic acid molecule encoding a calcium-binding protein is used in preventing, treating or ameliorating a medical condition .

Claim 11: SEQ ID No 149; 542bp; English.

The present invention relates to the isolation of novel human calcium-binding proteins, and cDNA (AAS31577-AAS31654) and genomic sequences encoding for these proteins. The sequences of the invention are useful in the diagnosis, prevention and/or prognosis of diseases associated with aberrant calcium flux. Such disorders include neurological diseases (e.g. amyotrophic lateral sclerosis, ALS), immune dysfunction (e.g. severe combined immunodeficiency, SCID), digestive disorders (e.g. irritable bowel syndrome, IBS), neoplastic disease (e.g. cancer), blood disorders (e.g. haemophilia), and/or infectious disease (e.g. acquired immunodeficiency syndrome, AIDS). The novel calcium-binding proteins are also useful as screening tools to identify antagonists and/or agonists that may enhance or inhibit activities mediated by calcium-binding proteins. The polynucleotides of the invention are also useful in gene therapy. AAU19897-AAU19966 represent the novel human calcium-binding proteins.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pat_sequences.

Sequence 173 AA:

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Best Local Similarity 38.9%; Pred. NO. 5.4e-23;  
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13 LAEYODTFLKQELLAHRRFCCLPDEQRVTSSSLAAQVFEEDISLPELKANPKFR 72  
| | | | | | | | | | | | : : : : :  
: : : | | | | : | | | |
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D b      I LEEVQALFTLRNELLCHIDFLFKLPCKYKKEKL--TMOVSSPLRLNPNPRDR 56
O y      73 ICVESTSPAKDLSLEDFDLILSVSDATADISHTAFRFDPDDGGITNRBDSLRY 132
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D b      57 ICNFVS---HKGFSEFDVGMAVSFSEACPSLIEFAFRITRDENGEFIIDEEDLORII 113
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O y      133 NCUTGECEDTRLASSEMOKOLIDILEEXXXXXXXXXXXXXXOHYIANSPPAFSFF 187
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AC	AAE09736 standard; Protein; 187 AA.
XX	AAE09736;
DT	29-NOV-2001 (first entry)
XX	
DE	Human kinase interacting protein.
XX	
KW	Human; kinase interacting protein; novel human protein; NHP;
XX	gene therapy; drug screening; mental disorder; biological disorder;
KW	medical disease; noctropic.
XX	
OS	Homo sapiens.
XX	
PN	WO20016760-A2.
PD	13-SEP-2001.
XX	
XX	08-MAR-2001; 2001WO-US07499.
XX	
PR	08-MAR-2000; 2000US-0187719.
XX	
PA	(LEXI-) LEXICON GENETICS INC.
XX	
PI	Mathur B, Turner CA;
XX	
DR	WPI; 2001-557870/62.
DR	N-PSDB; AAD16796.
XX	
PT	Novel polynucleotides encoding human kinase interacting protein useful
PT	for drug screening, diagnosis and in gene therapy of biological
PT	disorders .
PS	
PS	Claim 2; Page 31-32; 32pp; English.
XX	
CC	The present amino acid sequence is a novel human protein (NHP),
CC	human kinase interacting protein. NHP oligonucleotides are useful
CC	as hybridisation probes for screening libraries and assessing gene
CC	expression patterns. Sequences derived from regions adjacent to the
CC	intron/exon boundaries of NHP gene are used to design primers for
CC	use in amplification assays to detect mutations within the exons,
CC	splice sites, introns that can be used in diagnostics and
CC	pharmacogenomics. NHP nucleotide sequences are useful for drug
CC	screening and nucleotide construct encoding NHP products are
CC	useful in gene therapy for modulating NHP expression and to produce
CC	genetically engineered host-cells to express NHP products in vivo.
CC	The encoded NHP polypeptides are useful for generating antibodies,
CC	as reagents in diagnostic assays, for identifying other cellular
CC	gene products related to NHP and as reagents in assays for screening
CC	or medical disorders and diseases.
XX	
XX	Sequence 187 AA;

	Query Match	35.8%	Score 324;	DB 22..	Length 187;
	Best Local Similarity	37.3%	Pred. No. 9.8e-23;		
	Matches 72; Conservative	52;	Mismatches 50;	Indels 12;	Gaps 5
OY	1 MGSGSLSKELLERYODLPFLTKOEILLANRPCELLP----	EQRVSSLRQVPFE	56		
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Db 1 MGNKQVFTHEOLEAYODCTFFTRKEIMLFYQDLAPOLVLDYTCPD---VAVPYE 57
 QY 57 QILSLPELKANPEKRICVFTSPAKDSLSEDFDLISVSDATPPIKSHYARIPD 116
 Db 58 LIGSMPELNDNPFROIAQVFS-EDGDGHNTLDNFMFSVSEMAPRDLKAYAFKIYD 116
 QY 117 FDDGTLNREDLSRLVNCITGEGEDTRLASASEMKOLIDNILEEXXXXXXXXXXQHVV 176
 Db 117 FNNDDYICAMDELEQVTKLT-RGE---LSAEVSLVCEKYLDEADGDHGRSLSEDFQNM 172
 QY 177 ISRSPDFASSFKI 189
 Db 173 ILRAPDFLSTFHI 185

RESULT 14
 ABG30437
 ID ABG30437 standard; Protein; 187 AA.
 AC ABG30437;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Human protein sequence #5 used for determining sequence of unknown gene.
 XX
 KW Human; sequence determination.
 XX
 OS Homo sapiens.
 XX
 PN JP2002176980-A.
 XX
 PD 25-JUN-2002.
 XX
 PF 12-DEC-2000; 2000JP-0377888.
 XX
 PR 12-DEC-2000; 2000JP-0377888.
 XX
 PA (AISE) AISIN SEIKI KK.
 XX
 PA (MEIZ) MEIZU KK.
 XX
 DR WPI; 2002-569942/61.
 DR N-PSDB; ABR88216.
 XX
 PT Provisionary determination of an unknown gene sequence by using known
 PT gene sequence data, Expressed Sequence Tag data and genomic data
 XX
 PS Disclosure; Fig 2; 13pp; Japanese.
 XX
 CC This invention relates to a method for determination of an unknown gene
 CC sequence by using a database of known gene sequences, Expressed Sequence
 CC Tag (EST) sequences and genomic sequences including a step in which the
 CC homology is searched from the known gene sequence contained in the
 CC database and known EST sequence to get a first consensus sequence and
 CC from this to construct a database of the first consensus sequence.
 CC The methods of the invention are used for the provisional determination
 CC of an unknown gene sequence. The present sequence represents a
 CC human protein sequence used in an example of the method of the
 CC invention to determine the sequence of an unknown gene.
 CC
 SQ Sequence 187 AA;

Query Match 35.8%; Score 324; DB 23; Length 187;
 Best Local Similarity 37.3%; Pred. NO. 9.8e-23;
 Matches 72; Conservative 52; Mismatches 57; Indels 12; Gaps 5;

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 QY 57 QILSLPELKANPEKRICVFTSPAKDSLSEDFDLISVSDATPPIKSHYARIPD 116
 Db 58 LIGSMPELNDNPFROIAQVFS-EDGDGHNTLDNFMFSVSEMAPRDLKAYAFKIYD 116

QY 117 FDDGTLNREDLSRLVNCITGEGEDTRLASASEMKOLIDNILEEXXXXXXXXXXQHVV 176
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 QY 177 ISRSPDFASSFKI 189
 Db 173 ILRAPDFLSTFHI 185

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 ID ABB64325 standard; Protein; 206 AA.
 AC ABB64325;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 19767.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US09231.
 XX
 PR 23-MAR-2000; 2000US-191637P.
 XX
 PR 11-JUL-2000; 2000US-0614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 XX Venter JC, Adams M, Li PWD, Myers EW;
 XX WPI; 2001-656860/75.
 XX DR N-PSDB; ABL08428.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions.
 XX
 PS Disclosure; SEQ ID NO 19767; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABBS7737-ABR2072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 CC
 SQ Sequence 206 AA;

Query Match 35.2%; Score 318.5; DB 22; Length 206;
 Best Local Similarity 40.9%; Pred. NO. 4.1e-22;
 Matches 72; Conservative 39; Mismatches 46; Indels 17; Gaps 5;

QY 17 QDLFLTKOELLARHRCCELLPQ---EQRVSESLAQAQVPEQILSPPELKANPEKRI 73
 Db 43 KDCFFTRKEIMLFYQDLAPOLVLDYTCPD---VAVPYE 57
 QY 74 CRVFTSPAKDSLSEDFDLISVSDATPPIKSHYARIPD 116
 Db 95 -EAFSRD-GQGNLSFEDLDLISVSEQAPRDIKVFYAFKIYDFDQDFIGHAD---LMS 149
 QY 134 CITGEGEDTRLASASEMKOLIDNILEEXXXXXXXXXXQHVVISRSPDFASSFKI 189

Db 150 CLTMTKN-ELSPBEHQIADKYIEADVDGDKLSILPEPHVILRAPDFLSTFHI 204

Search completed: July 24, 2003, 13:16:23
Job time : 87 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 24, 2003, 12:55:52 ; Search time 29 Seconds

(without alignments)
278.668 Million cell updates/sec

Title: SEQ2_MOD

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Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	876	96.8	191	3	US-08-764-563-1
3	195.5	21.6	177	3	US-08-764-563-3
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30	122.5	13.5	270	4	US-09-399-913-14	Sequence 14, Appl
31	122.5	13.5	270	4	US-09-298-731-14	Sequence 14, Appl
32	120.5	13.3	216	4	US-09-399-913-6	Sequence 6, Appl
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34	120.5	13.3	227	4	US-09-399-913-8	Sequence 8, Appl
35	120.5	13.3	227	4	US-09-399-913-8	Sequence 8, Appl
36	120.5	13.3	227	4	US-09-399-913-10	Sequence 10, Appl
37	120.5	13.3	227	4	US-09-298-731-8	Sequence 8, Appl
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ALIGNMENTS

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RESULT 1
US-08-720-625-2
Sequence 2, Application US/08720625
Patent No. 6242587
GENERAL INFORMATION:
APPLICANT: Naik, Ulhas P.
TITLE OF INVENTION: CALCIUM-INTERGRIN BINDING PROTEIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSES:
ADDRESS: Bell, Seltzer, Park & Gibson
STREET: P.O. Drawer 34009
CITY: Charlotte
STATE: No. 6242587th Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/720,625
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5470-138
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-720-625-2
Query Match 99.6% Score 901, DB 3, Length 191:
Best Local similarity 92.1% Pred. No. 3e-89; 0: Indels 0: Gaps 0:
Matches 176: Conservative 15: Mismatches
```

1 MGSGSRLSKELLAEDLFTLTKOELLARRCCELLPOORTVSSLRQVFEOLLS 60
|||||
1 MGSGSRLSKELLAEDLFTLTKOELLARRCCELLPOORTVSSLRQVFEOLLS 60
|||||
61 LPELKANPFRICRIVSTSPAKDSLFEDELILSVFSDATPDIKSHVAFRIFDEPDD 120
|||||

Db 61 LPELKNPFRKICRVSTSPAKDSLSFEDFLDLVSFSDTAPDRIKSHYAFRIFPD 120
QY 121 GTLNREDLSRLVNCITGEGEDTRLASSEMQLIDNILEEXXXXXXXXXXQHVIYSRS 180
Db 121 GTLNREDLSRLVNCITGEGEDTRLASSEMQLIDNILEESDIDRDGTINLSEFOHYISRS 180
QY 181 PDFASSFKIVL 191
Db 181 PDFASSFKIVL 191

RESULT 2
US-08-764-563-1
; Sequence 1, Application US/08764563
; Patent No. 6093565
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: A NOVEL PROTEIN PHOSPHATASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/764,563
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0178 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 191 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: Consensus
; CLONE: Consensus
; US-08-764-563-1

Query Match 96.8%; Score 876; DB 3; Length 191;
Best Local Similarity 91.6%; Pred. No. 1.5e-86;
Matches 175; Conservative 14; Mismatches 2; Indels 0; Gaps 0;

QY 1 MCGSGSRLSKELLAEOVDITFLTKOETLAHRRFCCLLPQEOQRTVSSSLRAQVPEQIILS 60
Db 1 MCGSGSRLSKELLAEOVDITFLTKOETLAHRRFCCLLPQEOQRTVSSSLRAQVPEQIILS 60
QY 61 LPELKNPFRKICRVSTSPAKDSLSFEDFLDLVSFSDTAPDRIKSHYAFRIFPD 120
Db 61 LPELKNPFRKICRVSTSPAKDSLSFEDFLDLVSFSDTAPDRIKSHYAFRIFPD 120
QY 121 GTLNREDLSRLVNCITGEGEDTRLASSEMQLIDNILEEXXXXXXXXXXQHVIYSRS 180
Db 121 GTLNREDLSRLVNCITGEGEDTRLASSEMQLIDNILEESDIDRDGTINLSEFOHYISRS 180

QY 181 PDFASSFKIVL 191
Db 181 PDFASSFKIVL 191

RESULT 3
US-08-764-563-3
; Sequence 3, Application US/08764563
; Patent No. 6093565
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: A NOVEL PROTEIN PHOSPHATASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/764,563
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0178 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: Genbank
; CLONE: 458230
; US-08-764-563-3

Query Match 21.6%; Score 195.5; DB 3; Length 177;
Best Local Similarity 25.3%; Pred. No. 1.1e-12;
Matches 45; Conservative 52; Mismatches 68; Indels 13; Gaps 3;

QY 1 MCGSGSRLSKELLAEOVDITFLTKOETLAHRRFCCLLPQEOQRTVSSSLRAQVPEQIILS 60
Db 1 MCGNTSSLRREVEEMQKGNFTOKELKIKYKFKIKDKGNGTISK-----DEFLM 52
QY 61 LPELKNPFRKICRVSTSPAKDSLSFEDFLDLVSFSDTAPDRIKSHYAFRIFPD 120
Db 53 IPELAVNPVLRKIVSIFDEN-GDGSVNFKEFIALSVFNQGDQKORLEAFVYDIDGD 111
QY 121 GTLNREDLSRLVNCITGEGEDTRLASSEMQLIDNILEEXXXXXXXXXXQHVIYS 178
Db 112 GYISNGLFTVLKMWG---NNLSOVQLOQIVDKTITLEADEDGDGKISFEPAKTLIS 165

RESULT 4
US-08-328-322-17
; Sequence 17, Application US/08328322

```
Patent No. 5723436
GENERAL INFORMATION:
APPLICANT: Huang, Laiqiang
APPLICANT: Cyert, Martha S.
TITLE OF INVENTION: Calcineurin Interacting Protein Compositions
TITLE OF INVENTION: and Methods
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
City: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,322
FILING DATE: 24-OCT-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: P38,615
REFERENCE/DOCKET NUMBER: 8600-0151.10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-328-322-17

Query Match
Best Local Similarity: 20.4%; Score 184.5; DB 1; Length 174;
Matches 42; Conservative 55; Mismatches 63; Indels 17; Gaps 4;

QY 1 MGSQSGSKEDLAEXODLFTLKQELLAHRRFCELLPQEQRTVSSLRQVPEQILSPAK 60
DB 1 MGAAPSKIYDGLLED---TNRDREIELRRKRMKLDSSGSIDKN-----EFMS 48
QY 61 LPELANPPEKRICRVFSTSPAKDSISEFEDLDLVSFSDTATPDIKSHYAFRIEDFDD 120
DB 49 IGVSSNPPLAGRIIMEVFADNSGD-VDFQEFITGLSIFSGSGSKDEKLFARFIYDIDKD 107
QY 121 GTLNREDLSRLVNCITLGEDEGTRLSASEMKOLIDNILEXXXXXXXHXOHI 177
DB 108 GTSINGELFTYLVKIMG---SNLDEQLQQLVDRITVENSDSDGGRSLSEEFKNAI 160

RESULT 5
US-08-328-322-15
Sequence 15, Application US/08328322
Patent No. 5723436
GENERAL INFORMATION:
APPLICANT: Huang, Laiqiang
APPLICANT: Cyert, Martha S.
TITLE OF INVENTION: Calcineurin Interacting Protein Compositions
TITLE OF INVENTION: and Methods
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
City: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
```

```
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,322
FILING DATE: 24-OCT-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: P38,615
REFERENCE/DOCKET NUMBER: 8600-0151.10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-328-322-15

Query Match
Best Local Similarity: 19.2%; Score 173.5; DB 1; Length 157;
Matches 36; Conservative 51; Mismatches 54; Indels 13; Gaps 3;

QY 24 KOELLAHRRFCELLPQEQRTVSSLRQVPEQILSPKLANPKEKICRVFSTSPAK 83
DB 3 RDEIERLRKRRFMKLDSSGSIDKN-----EFMSIPVSSNPPLAGRIIMEVFADNSG 54
QY 84 DSISEFEDLDLVSFSDTATPDIKSHYAFRIEDFDDGTNLNEDLSRLVNCITLGEDE 143
DB 55 D-VDFQEFITGLSIFSGSGSKDEKLFARFIYDIDKDGFSINELFTYLVKIMG---SN 109
QY 144 LSASEMKOLIDNILEXXXXXXXHXOHI 177
DB 110 LDEQLQQLVDRITVENSDSDGGRSLSEEFKNAI 143

RESULT 6
US-08-720-625-4
Sequence 4, Application US/08720625
Patent No. 6242587
GENERAL INFORMATION:
APPLICANT: Naik, Ulhas P.
APPLICANT: Parise, Leslie V.
TITLE OF INVENTION: CALCIUM-INTEGRIN BINDING PROTEIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell, Seltzer, Park & Gibson
STREET: P.O. Drawer 34009
City: Charlotte
STATE: No. 6242587th Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/720,625
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5470-138
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 4:
```

QY 1 MGSGSRUSKELLAEYODLFTLTKEILLAHRRFCCLLPQEORTVSSSLRAQVPFEQILS 60
11 :
Db 1 MGKSSSKLKODITRLTDTDYETEKETIROMHKGFLKDCPNGLLTBEGGFIKIYKOF---- 55

QY 61 LPELKANPFKERICRVFSTSPAKDSLSEDFDLILSVESDTPATPIKSHYAFRIEDFDD 120
 DB 56 FPOGDPKSFASLVFVFDEN-NDGSIIEFEERFIALSVYSGU--DEKLOMAFRLYDND 112
 QY 121 GTLNREDLSRLVNCI-----TGEGEDTRLASSEMOKOLIDNILEEXXXXXXXXXXXX 172
 DB 113 GYITREEMYNIVDAIYQVGOQPOSEDENT-----PKRVKDKIFDQMDKNHDKLTLEE 166
 QY 173 XOHVISRSPDPFASFRI 189
 DB 167 FREGSKADPRIVQALSL 183

RESULT 9
 US-09-258-016-8
 Sequence 8, Application US/09258016
 Patent No. 6362395

GENERAL INFORMATION:
 APPLICANT: Bachettira W. Poovalah, Zhinhua Liu,
 APPLICANT: Shameekumar Patil, Daisuke Takezawa
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
 PRODUCTION OF MALE-STERILE PLANTS
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Klargust Sparkman Campbell Leigh &
 ADDRESSEE: Whinston, LLP
 STREET: One World Trade Center
 STREET: 121 S.W. Salmon Street
 CITY: Portland
 STATE: Oregon
 COUNTRY: United States of America
 ZIP: 97204

COMPUTER READABLE FORM:
 MEDIUM TYPE: Disk, 3-1/2 inch
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: MS DOS
 SOFTWARE: WordPerfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/258.016
 FILING DATE:

ATTORNEY/AGENT INFORMATION:
 NAME: Stephens Jr., Donald L.
 REGISTRATION NUMBER: 34,022
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (503) 226-7391
 TELEFAX: (503) 228-9446
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 186 amino acids
 TYPE: amino acid

MOLECULE TYPE: protein
 DESCRIPTION: Region of Drosophila frequency
 DESCRIPTION: (Gen2:Proteog) with homology to 111y
 DESCRIPTION: CCAAK
 US-09-258-016-8

Query Match 17.6%; Score 159; DB 4; Length 186;
 Best Local Similarity 22.3%; Pred. No. 1.1e-08;
 Matches 44; Conservative 52; Mismatches 79; Indels 22; Gaps 5;

QY 1 MGGSGSRSLKELLAEYODLFTLTKOELLAHRRFCCELLPOQRRTVESSLRAQVPEEILS 60
 DB 1 MGKSSKIKQDITDLTDITFTKEIKRQWKGFLKDCPNGLITGOGFIYKOF----- 55
 QY 61 LPELKANPFKERICRVFSTSPAKDSLSEDFDLILSVESDTPATPIKSHYAFRIEDFDD 120
 DB 56 FPOGDPKSFASLVFVFDEN-NDGSIIEFEERFIALSVYSGU--DEKLOMAFRLYDND 112

QY 121 GTLNREDLSRLVNCI-----TGEGEDTRLASSEMOKOLIDNILEEXXXXXXXXXXXX 172
 DB 113 GYITREEMYNIVDAIYQVGOQPOSEDENT-----PKRVKDKIFDQMDKNHDKLTLEE 166
 QY 173 XOHVISRSPDPFASFRI 189
 DB 167 FREGSKADPRIVQALSL 183

RESULT 10
 US-09-257-825B-8
 Sequence 8, Application US/09257825B
 Patent No. 6403352

GENERAL INFORMATION:
 APPLICANT: Poovalah, Bachettira W.
 APPLICANT: Patil, Shameekumar
 APPLICANT: Takezawa, Daisuke
 TITLE OF INVENTION: Compositions and Methods for production of Male-Sterile Plants
 FILE REFERENCE: 4630-51993
 CURRENT APPLICATION NUMBER: US/09/257,825B
 CURRENT FILING DATE: 1999-02-25
 PRIOR APPLICATION NUMBER: US 08/655,352
 PRIOR FILING DATE: 1996-05-23
 PRIOR APPLICATION NUMBER: US 60/014,743
 NUMBER OF SEQ ID NOS: 28
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 8
 LENGTH: 186
 TYPE: PRT
 ORGANISM: Drosophila
 US-09-257-825B-8

Query Match 17.6%; Score 159; DB 4; Length 186;
 Best Local Similarity 22.3%; Pred. No. 1.1e-08;
 Matches 44; Conservative 52; Mismatches 79; Indels 22; Gaps 5;

QY 1 MGGSGSRSLKELLAEYODLFTLTKOELLAHRRFCCELLPOQRRTVESSLRAQVPEEILS 60
 DB 1 MGKSSKIKQDITDLTDITFTKEIKRQWKGFLKDCPNGLITGOGFIYKOF----- 55
 QY 61 LPELKANPFKERICRVFSTSPAKDSLSEDFDLILSVESDTPATPIKSHYAFRIEDFDD 120
 DB 56 FPOGDPKSFASLVFVFDEN-NDGSIIEFEERFIALSVYSGU--DEKLOMAFRLYDND 112
 QY 121 GTLNREDLSRLVNCI-----TGEGEDTRLASSEMOKOLIDNILEEXXXXXXXXXXXX 172
 DB 113 GYITREEMYNIVDAIYQVGOQPOSEDENT-----PKRVKDKIFDQMDKNHDKLTLEE 166
 QY 173 XOHVISRSPDPFASFRI 189
 DB 167 FREGSKADPRIVQALSL 183

RESULT 11
 US-08-764-563-4
 Sequence 4, Application US/08764563
 Patent No. 6093565

GENERAL INFORMATION:
 APPLICANT: Hillman, Jennifer L.
 APPLICANT: Goli, Surya K.
 TITLE OF INVENTION: A NOVEL PROTEIN PHOSPHATASE
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,563
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0178 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 179 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 109612
US-08-764-563-4

Query Match 17.1%; Score 154.5; DB 3; Length 179;
Best Local Similarity 23.2%; Pred. No. 3.2e-08;
Matches 33; Conservative 43; Mismatches 60; Indels 13; Gaps 3;

QY 35 CELLPORO-----RTVSSSLRAOVFPFOILSLPELKANPFRICRVFSPANDSL 86
DB 12 CNHDOEIRLKGSPFKLDKSGSLSEFPMPLQONPLVGRVIDFDID-NGEYV 70
QY 87 SEFDLDLVSFSDTAPDPIKSHYAFRIPEDDGTINREDLSLVNCLTGEGETRLSA 146
DB 71 DFHEFIYGTSGFSYKGEQKLRFAFRITYMDNDGFIISNGLQVLMKMG---NNLKD 126
QY 147 SENKQLDNILEEXXXXXXXXXXXXXQHYI 177
DB 127 WOLQOVLVKSILVLDKDGRISEFSDVY 157

RESULT 12
US-09-048-889-1
Sequence 1, Application US/09048889

GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Lal, Preeti
APPLICANT: Patterson, Chandra
TITLE OF INVENTION: HUMAN CALCIUM-BINDING PROTEINS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/048,889
FILING DATE: Herewith

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Ceirone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0493 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 196 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: COLN00709
CLONE: 1846517
US-09-048-889-1

Query Match 14.9%; Score 134.5; DB 3; Length 196;
Best Local Similarity 20.1%; Pred. No. 5.7e-06;
Matches 38; Conservative 50; Mismatches 68; Indels 33; Gaps 6;

QY 5 GSRLSKELAEYODL-----TEFLKOEILAHRRCELLPOEORTVSSSLRAQVFEQILS 60
DB 2 GSRISHAAYIPDGSIRRETGFSQASILRLHFR-----RALDRKKGYLSRMDLQ 53
QY 61 LPELKANPFRICRVSTSPAKDSSEFDLDSVF-----SDTATPIKS----- 108
DB 54 IGAIVNPLDRIIESFPG-GSORVDPPGVRLAHFRVEDEDTOTDPKKEPLNSR 112
QY 109 ----HYAFRIPEDDGTINREDLSLVNCLTGEGETRLSASEMKQLDNILEEXXXXX 164
DB 113 RNLHVAFOLYLDIDROCKISRHEMLQVLRIMVG----VQTEEDLENIAQRTVQENEDG 168
QY 165 XXXXXXXXX 173
DB 169 DGAVSEVEF 177

RESULT 13
US-08-655-352-3
Sequence 3, Application US/08655352

GENERAL INFORMATION:
APPLICANT: Bachettira W. Poovalah, Zhihua Liu,
APPLICANT: Shameekumar Patil, Daisuke Takezawa
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
PRODUCTION OF MALE-STERILE PLANTS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kiarquist Sparkman Campbell Leigh &
STREET: Winston, LLP
STREET: One World Trade Center
STREET: 121 S.W. Salmon Street
STREET: Suite 1600
CITY: Portland
STATE: Oregon
COUNTRY: United States of America
ZIP: 97204
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/655,352
FILING DATE:
CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/323,449

FILING DATE: October 14, 1994

ATTORNEY/AGENT INFORMATION:

NAME: Dow, Alan. E.

REGISTRATION NUMBER: 35,123

TELECOMMUNICATION INFORMATION:

TELEPHONE: (503) 226-7391

TELEFAX: (503) 226-9446

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 193 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

DESCRIPTION: Region of rat neural visinin-like protein

DESCRIPTION: (Gen2:Ratnvp3) with homology to 11ly

US-08-655-352-3

Query Match 14.4%; Score 130.5; DB 3; Length 193;

Best Local Similarity 22.8%; Pred. No. 1.5e-05;

Matches 41; Conservative 50; Mismatches 72; Indels 17; Gaps 5;

QY 1 MGGSGSRSLKELLAEYODLFTLKQELLAHRRFCCLLPQEQRTVSSLRQVPEQILS 60

DB 1 MGKNSKLRPEVLQDLREHTEFTDHELOEWYKGLKDCPTGHLTVDE-----FKKIYA 53

QY 61 --LPELKANPFKERICRVSTSPAKDSLSFEDFDLDSVSDTATPDIKSHYAFRIFFD 118

DB 54 NEFPYGDASKFAEHVFRFTDIN-SDGTIDREFITALSVTS-RGKLEOKIKWAFSMYDLD 111

QY 119 DGGTLNRDLSRLVNCLTGEGEDTRLASSEMQLDNLLEEXXXXXXXXQHVIS 178

DB 112 GNGYISRSEMLEIVQAI-----YKVVSSVMKMPEDSTPEKRTDKIFROMDINNCKLS 165

RESULT 14

US-09-258-016-3

Sequence 3, Application US/09258016

Patent No. 6362395

GENERAL INFORMATION:

APPLICANT: Bachettira W. Poovaiyah, Zhinua Liu,

APPLICANT: Shameekumar Patil, Daisuke Takezawa

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR

TITLE OF INVENTION: PRODUCTION OF MALE-STERILE PLANTS

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Kiarquist Sparkman Campbell Leigh &

ADDRESSEE: Whinston, LLP

STREET: One World Trade Center

STREET: 121 S.W. Salmon Street

STREET: Suite 1600

CITY: Portland

STATE: Oregon

COUNTRY: United States of America

ZIP: 97204

COMPUTER READABLE FORM:

MEDIUM TYPE: Disk, 3-1/2 inch

COMPUTER: IBM PC compatible

OPERATING SYSTEM: MS DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/258, 016

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Stephens Jr., Donald L.

REGISTRATION NUMBER: 34,022

REFERENCE/DOCKET NUMBER: 4630-51994

TELECOMMUNICATION INFORMATION:

TELEPHONE: (503) 226-7391

TELEFAX: (503) 228-9446

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 193 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

DESCRIPTION: Region of rat neural visinin-like protein

DESCRIPTION: (Gen2:Ratnvp3) with homology to 11ly

DESCRIPTION: CCAMK

US-09-258-016-3

Query Match 14.4%; Score 130.5; DB 4; Length 193;

Best Local Similarity 22.8%; Pred. No. 1.5e-05;

Matches 41; Conservative 50; Mismatches 72; Indels 17; Gaps 5;

QY 1 MGGSGSRSLKELLAEYODLFTLKQELLAHRRFCCLLPQEQRTVSSLRQVPEQILS 60

DB 1 MGKNSKLRPEVLQDLREHTEFTDHELOEWYKGLKDCPTGHLTVDE-----FKKIYA 53

QY 61 --LPELKANPFKERICRVSTSPAKDSLSFEDFDLDSVSDTATPDIKSHYAFRIFFD 118

DB 54 NEFPYGDASKFAEHVFRFTDIN-SDGTIDREFITALSVTS-RGKLEOKIKWAFSMYDLD 111

QY 119 DGGTLNRDLSRLVNCLTGEGEDTRLASSEMQLDNLLEEXXXXXXXXQHVIS 178

DB 112 GNGYISRSEMLEIVQAI-----YKVVSSVMKMPEDSTPEKRTDKIFROMDINNCKLS 165

RESULT 15

US-09-257-825B-3

Sequence 3, Application US/09257825B

Patent No. 6403352

GENERAL INFORMATION:

APPLICANT: Poovaiyah, Shameekumar

APPLICANT: Patil, Shameekumar

TITLE OF INVENTION: Compositions and Methods for Production of Male-Sterile Plants

FILE REFERENCE: 4630-51993

CURRENT APPLICATION NUMBER: US/09/257, 825B

CURRENT FILING DATE: 1999-02-25

PRIOR APPLICATION NUMBER: US 08/655,352

PRIOR FILING DATE: 1996-05-23

PRIOR APPLICATION NUMBER: US 60/014,743

PRIOR FILING DATE: 1996-03-28

NUMBER OF SEQ ID NOS: 28

SOFTWARE: PatentIn version 3.1

SEQ ID NO 3

LENGTH: 193

TYPE: PRT

ORGANISM: Rat

US-09-257-825B-3

Query Match 14.4%; Score 130.5; DB 4; Length 193;

Best Local Similarity 22.8%; Pred. No. 1.5e-05;

Matches 41; Conservative 50; Mismatches 72; Indels 17; Gaps 5;

QY 1 MGGSGSRSLKELLAEYODLFTLKQELLAHRRFCCLLPQEQRTVSSLRQVPEQILS 60

DB 1 MGKNSKLRPEVLQDLREHTEFTDHELOEWYKGLKDCPTGHLTVDE-----FKKIYA 53

QY 61 --LPELKANPFKERICRVSTSPAKDSLSFEDFDLDSVSDTATPDIKSHYAFRIFFD 118

DB 54 NEFPYGDASKFAEHVFRFTDIN-SDGTIDREFITALSVTS-RGKLEOKIKWAFSMYDLD 111

QY 119 DGGTLNRDLSRLVNCLTGEGEDTRLASSEMQLDNLLEEXXXXXXXXQHVIS 178

DB 112 GNGYISRSEMLEIVQAI-----YKVVSSVMKMPEDSTPEKRTDKIFROMDINNCKLS 165

Search completed: July 24, 2003, 13:19:56

Job time : 30 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 24, 2003, 13:16:31 ; Search time 23 Seconds

(without alignments)
966.222 Million cell updates/sec

Title: SEQ2_MOD

Perfect score: 905
Sequence: 1 MGGSGSRSLKELLAETDYL.....XXQHVHSNPPFASSKIVL 191

Scoring table: BIOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 451899 seqs, 118759770 residues

Total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

Published Applications: AA:
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PC1_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PC1US_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09C_NEW_PUB.pep.*
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14: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
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17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	905	100.0	191	9	US-09-878-454A-2
2	893	98.7	191	14	US-10-109-885-2
3	342.5	37.8	201	11	US-09-992-600A-56
4	342.5	37.8	201	11	US-09-924-340-56
5	342.5	37.8	201	15	US-10-000-489-56
6	342.5	37.8	201	15	US-10-000-986-56
7	326	36.0	173	11	US-09-764-891-4020
8	326	36.0	173	11	US-09-764-891-149
9	324	35.8	187	9	US-09-802-116-2
10	165.5	18.3	170	14	US-10-109-885-3
11	162.5	18.0	195	9	US-09-999-602-3
12	157.5	17.4	195	9	US-09-999-602-4
13	157	17.3	214	9	US-09-999-602-1
14	157	17.3	257	15	US-10-106-698-6128
15	152	16.8	189	11	US-09-764-891-3897

152	16.8	189	11	US-09-764-881-148	Sequence 148, App
140.5	15.5	194	11	US-09-764-881-123	Sequence 123, App
133.5	14.8	207	11	US-09-764-881-145	Sequence 145, App
128.5	14.2	190	15	US-10-128-714-3360	Sequence 3360, Ap
127	14.0	220	9	US-09-350-874-26	Sequence 26, Appl
127	14.0	220	15	US-10-106-989-26	Sequence 26, Appl
123.5	13.6	190	15	US-10-128-714-8360	Sequence 8360, Ap
122.5	13.5	220	9	US-09-350-874-24	Sequence 24, Appl
122.5	13.5	220	15	US-10-106-989-24	Sequence 24, Appl
122.5	13.5	252	9	US-09-350-874-20	Sequence 20, Appl
122.5	13.5	252	15	US-10-106-989-20	Sequence 20, Appl
122.5	13.5	270	9	US-09-350-874-14	Sequence 14, Appl
122.5	13.5	270	15	US-10-106-989-14	Sequence 14, Appl
122.5	13.5	1210	10	US-09-833-263-692	Sequence 692, App
122.5	13.5	1210	14	US-10-025-380-692	Sequence 692, App
122.5	13.5	1548	9	US-09-922-217-1095	Sequence 1095, Ap
120.5	13.3	1548	14	US-10-025-380-1095	Sequence 1095, Ap
120.5	13.3	216	9	US-09-350-874-6	Sequence 6, Appl1
120.5	13.3	216	15	US-10-106-989-6	Sequence 6, Appl1
120.5	13.3	227	9	US-09-350-874-8	Sequence 8, Appl1
120.5	13.3	227	15	US-09-350-874-10	Sequence 8, Appl1
120.5	13.3	227	15	US-10-106-989-8	Sequence 10, Appl
120.5	13.3	227	15	US-10-106-989-10	Sequence 10, Appl
120.5	13.3	245	9	US-09-350-874-4	Sequence 4, Appl1
120.5	13.3	245	15	US-10-106-989-4	Sequence 4, Appl1
120.5	13.3	270	9	US-09-350-874-18	Sequence 18, Appl
120.5	13.3	270	15	US-10-106-989-18	Sequence 18, Appl
119.5	13.2	216	9	US-09-350-874-2	Sequence 2, Appl1
119.5	13.2	216	10	US-09-965-528-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-09-878-454A-2
Sequence 2, Application US/09878454A
Patent No. US20020064828A1
GENERAL INFORMATION:
APPLICANT: Monteiro, et al.
TITLE OF INVENTION: Method of Controlling the Binding of Calmyrin to Presenilin
FILE REFERENCE: 4115-161
CURRENT APPLICATION NUMBER: US/09/878, 454A
CURRENT FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: 60/210, 939
PRIOR FILING DATE: 2000-06-11
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 191
TYPE: PRT
ORGANISM: Homo sapiens
US-09-878-454A-2

Query Match 100.0%; Score 905; DB 9; Length 191;
Best Local Similarity 92.7%; Pred. No. 8.1e-81;
Matches 177; Conservative 14; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGGSGSRSLKELLAETDYLFLTRKQELLAAHRRCELLPORQTVESSLRAQVFEQILS 60
DB 1 MGGSGSRSLKELLAETDYLFLTRKQELLAAHRRCELLPORQTVESSLRAQVFEQILS 60
QY LPELKANPFRERICRWFSTSPAKDSLSFEDLILSVSPATPDISHVAFRIFDDDD 120
DB LPELKANPFRERICRWFSTSPAKDSLSFEDLILSVSPATPDISHVAFRIFDDDD 120
QY 121 GTINREDLSRLVNCITGEGEDTRLASSEMQLDNIIEEXXXXXXXXHHVHSRS 180
DB 121 GTINREDLSRLVNCITGEGEDTRLASSEMQLDNIIEESDIDRGTINISFOHVHSRS 180
QY 181 PDASSSKIVL 191
DB 181 PDASSSKIVL 191

DB 181 PDFASSFKIVL 191

RESULT 2

US-10-109-885-2

Sequence 2, Application US/10109885

Publication No. US20020119129A1

GENERAL INFORMATION:

APPLICANT: REVEL, Michel

APPLICANT: CHEBATH, Judith

APPLICANT: ABRAMOVITCH, Carolina

TITLE OF INVENTION: NOVEL IN RECEPTOR I BINDING PROTEIN, DNA ENCODING THEM, AND METHOD OF INVENTION: MODULATING CELLULAR RESPONSE TO INTERFERON

FILE REFERENCE: REVEL-14A

CURRENT APPLICATION NUMBER: US/10/109,885

PRIOR FILING DATE: 2002-04-01*

PRIOR APPLICATION NUMBER: US/09/341,640

PRIOR FILING DATE: 1999-10-18

PRIOR APPLICATION NUMBER: PCT/US98/00671

PRIOR FILING DATE: 1998-01-15

PRIOR APPLICATION NUMBER: US 60/035,636

PRIOR FILING DATE: 1997-01-15

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PatentIn version 3.1

SEQ ID NO 2

LENGTH: 191

TYPE: PRT

ORGANISM: Homo sapiens

US-10-109-885-2

Query Match

Best Local Similarity 98.7%; Score 893; DB 14; Length 191;

Matches 175; Conservative 15; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGGGSRSLKELAEYDQTLFTKOEILLARHRCCELLPOQRVSSSLRAQVPEQILS 60

DB 1 MGGGSRSLKELAEYDQTLFTKOEILLARHRCCELLPOQRVSSSLRAQVPEQILS 60

QY 61 LPELKANPFKERICRVSTSPAKDLSFEDEFLDLVSFSDTATPDIKSHVAFRIFFDDDD 120

DB 61 LPELKANPFKERICRVSTSPAKDLSFEDEFLDLVSFSDTATPDIKSHVAFRIFFDDDD 120

QY 121 GTLNREDLSRLVNLGTGEGEDTRLASSEMKNIDNILEEXXXXXXXHOHVISRS 180

DB 121 GTLNREDLSRLVNLGTGEGEDTRLASSEMKNIDNILEEXXXXXXXHOHVISRS 180

QY 181 PDFASSFKIVL 191

DB 181 PDFASSFKIVL 191

RESULT 3

US-09-992-600A-56

Sequence 56, Application US/09992600A

Publication No. US20030027161A1

GENERAL INFORMATION:

APPLICANT: Bejani, Stephanie

APPLICANT: Tanaka, Hiroaki

TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF

FILE REFERENCE: 91.US4.DIV

CURRENT APPLICATION NUMBER: US/09/992,600A

PRIOR FILING DATE: 2001-11-13

PRIOR APPLICATION NUMBER: US 09/924,340

PRIOR FILING DATE: 2001-08-06

PRIOR APPLICATION NUMBER: PCT/IB01/01715

PRIOR FILING DATE: 2001-08-06

PRIOR APPLICATION NUMBER: US 60/305,456

PRIOR FILING DATE: 2001-07-13

PRIOR APPLICATION NUMBER: US 60/302,277

PRIOR FILING DATE: 2001-06-29

PRIOR APPLICATION NUMBER: US 60/298,698

PRIOR FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: US 60/293,574

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 114

SOFTWARE: JPatent

SEQ ID NO 56

LENGTH: 201

TYPE: PRT

ORGANISM: Homo sapiens

US-09-992-600A-56

Query Match

Best Local Similarity 37.8%; Score 342.5; DB 11; Length 201;

Matches 73; Conservative 49; Mismatches 54; Indels 13; Gaps 4;

QY 1 MGGGSRSLKELAEYDQTLFTKOEILLARHRCCELLPOQRVSSSLRAQVPEQILS 60

DB 21 MNGVDTSLCDLL--QALFTLTREILCHIDFTLCPKRYKKEATL---TMDQVSS 73

QY 61 LPELKANPFKERICRVSTSPAKDLSFEDEFLDLVSFSDTATPDIKSHVAFRIFFDDDD 120

DB 74 LPAIRVNPFRICRVSTSPAKDLSFEDEFLDLVSFSDTATPDIKSHVAFRIFFDDDD 120

QY 121 GTLNREDLSRLVNLGTGEGEDTRLASSEMKNIDNILEEXXXXXXXHOHVISRS 180

DB 131 GFIDEEDLQRIITRLNLSDD--MSEDLMDLTNHLVSESDLDNDNMLSFSEFHAMAKS 187

QY 181 PDFASSFKI 189

DB 188 PDFMNSFKI 196

RESULT 4

US-09-924-340-56

Sequence 56, Application US/09924340

Publication No. US20030027248A1

GENERAL INFORMATION:

APPLICANT: Bejani, Stephanie

APPLICANT: Tanaka, Hiroaki

TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF

FILE REFERENCE: 91.US2.REG

CURRENT APPLICATION NUMBER: US/09/924,340

PRIOR FILING DATE: 2001-08-06

PRIOR APPLICATION NUMBER: US 60/305,456

PRIOR FILING DATE: 2001-07-13

PRIOR APPLICATION NUMBER: US 60/302,277

PRIOR FILING DATE: 2001-06-29

PRIOR APPLICATION NUMBER: US 60/298,698

PRIOR FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: US 60/293,574

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 112

SOFTWARE: JPatent

SEQ ID NO 56

LENGTH: 201

TYPE: PRT

ORGANISM: Homo sapiens

US-09-924-340-56

Query Match

Best Local Similarity 37.8%; Score 342.5; DB 11; Length 201;

Matches 73; Conservative 49; Mismatches 54; Indels 13; Gaps 4;

QY 1 MGGGSRSLKELAEYDQTLFTKOEILLARHRCCELLPOQRVSSSLRAQVPEQILS 60

DB 21 MNGVDTSLCDLL--QALFTLTREILCHIDFTLCPKRYKKEATL---TMDQVSS 73

QY 61 LPELKANPFKERICRVSTSPAKDLSFEDEFLDLVSFSDTATPDIKSHVAFRIFFDDDD 120

DB 74 LPAIRVNPFRICRVSTSPAKDLSFEDEFLDLVSFSDTATPDIKSHVAFRIFFDDDD 120

QY 121 GTLNREDLSRLVNLGTGEGEDTRLASSEMKNIDNILEEXXXXXXXHOHVISRS 180

DB 131 GFIDEEDLQRIITRLNLSDD--MSEDLMDLTNHLVSESDLDNDNMLSFSEFHAMAKS 187

QY 181 PDFASFKI 189
Db 188 PDFMNSFRI 196

RESULT 5

US-10-000-489-56
Sequence 56, Application US/10000489
Publication No. US20030092011A1
GENERAL INFORMATION:
APPLICANT: Benjamin, Stephanie
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.US6.DIV
CURRENT APPLICATION NUMBER: US/10/000,489
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: US 09/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: PCT/IB01/01715
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 112
SOFTWARE: Jpatent
SEQ ID NO 56
LENGTH: 201
TYPE: PRT
ORGANISM: Homo sapiens
US-10-000-489-56

Query Match

Best Local Similarity 37.8%; Score 342.5; DB 15; Length 201;
Matches 73; Conservative 49; Mismatches 54; Indels 13; Gaps 4;

QY 1 MCGSSGRLSKELLAEYODTLFLTKOEILLAHRRFCELLPOEORTVESSLRAQVPEOILS 60
Db 21 MNGVDTSLICDL--QALFLTRNEILCIHDTFLKCPGKYKENTL---TMDQVSS 73
QY 61 LPELKNPFRKERICRVFSTSPAKDSLFEFDLILSVSDTATPDIKSHYAFRIEDDD 120
Db 74 LPAALVNPFRDRIKRVFS--HKGMFSFEDVLGMASVSEQACPSLKIETVAFRIYDENEN 130
QY 121 GTLNREDLSRLVNCITGEGEDTRLASSEMOLINDNILEEXXXXXXXXQXHVISRS 180
Db 131 GFIDEEDLORITRLRLNSDD--MSDDLMDLTNHLVLSSESDIDNDNMLSFSEFEHAMAKS 187
QY 181 PDFASFKI 189
Db 188 PDFMNSFRI 196

RESULT 6

US-10-000-986-56
Sequence 56, Application US/10000986
Publication No. US20030096247A1
GENERAL INFORMATION:
APPLICANT: Benjamin, Stephanie
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.US9.DIV
CURRENT APPLICATION NUMBER: US/10/000,986
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: US 09/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: PCT/IB01/01715
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/305,456

PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 112
SOFTWARE: Jpatent
SEQ ID NO 56
LENGTH: 201
TYPE: PRT
ORGANISM: Homo sapiens
US-10-000-986-56

Query Match

Best Local Similarity 37.8%; Score 342.5; DB 15; Length 201;
Matches 73; Conservative 49; Mismatches 54; Indels 13; Gaps 4;

QY 1 MCGSSGRLSKELLAEYODTLFLTKOEILLAHRRFCELLPOEORTVESSLRAQVPEOILS 60
Db 21 MNGVDTSLICDL--QALFLTRNEILCIHDTFLKCPGKYKENTL---TMDQVSS 73
QY 61 LPELKNPFRKERICRVFSTSPAKDSLFEFDLILSVSDTATPDIKSHYAFRIEDDD 120
Db 74 LPAALVNPFRDRIKRVFS--HKGMFSFEDVLGMASVSEQACPSLKIETVAFRIYDENEN 130
QY 121 GTLNREDLSRLVNCITGEGEDTRLASSEMOLINDNILEEXXXXXXXXQXHVISRS 180
Db 131 GFIDEEDLORITRLRLNSDD--MSDDLMDLTNHLVLSSESDIDNDNMLSFSEFEHAMAKS 187
QY 181 PDFASFKI 189
Db 188 PDFMNSFRI 196

RESULT 7

US-09-764-891-4020
Sequence 4020, Application US/09764891
Publication No. US20030077808A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 10231
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4020
LENGTH: 173
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (137)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (168)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-891-4020

Query Match

Best Local Similarity 36.0%; Score 326; DB 11; Length 173;
Matches 68; Conservative 46; Mismatches 51; Indels 10; Gaps 3;

QY 13 LAEYODTLFLTKOEILLAHRRFCELLPOEORTVESSLRAQVPEOILSPLEKPNPKER 72
Db 1 LEEYQALFLTRNEILCIHDTFLKCPGKYKENTL---TMDQVSSLPALRVNPFDR 56
QY 73 ICRVSTSPAKDSLFEFDLILSVSDTATPDIKSHYAFRIEDDDGTLNREDLSRLV 132
Db 57 ICRVFS--HKGMFSFEDVLGMASVSEQACPSLKIETVAFRIYDENENGFIDEEDLORIT 113

QY 133 NCLTGEDETRLSASEMKQIDNILEEXXXXXXXXXXXXXXOIVSRSPDPASSF 187
DB 114 LRLNLSDD---MSEDLMLDITNHVLSXSDLDNDNMLSEFEFHAKAKSPDEFWTFP 165

RESULT 8
US-09-764-881-149
; Sequence 149, Application US/09764881
; Publication No. US20030125246A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT207
; CURRENT APPLICATION NUMBER: US/09/764,881
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 149
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (137)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (168)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-881-149

Query Match
Best Local Similarity 36.0%; Score 326; DB 11; Length 173;
Matches 68; Conservative 46; Mismatches 51; Indels 10; Gaps 3;
QY 133 LAEYODLFLTRKOEILLAHRRFCCELLPOEORTVESSLRAQVPEOILSPETKANPFKER 72
DB 1 LEEYGALFLTRNELLCHIDFLKCPCKYKENTL---TMDVSSLPALRVNPFRRR 56
QY 73 ICRVSTSPAKSLSFEDELILSVSDTAPDIKSHAFRIEDDDGTLNREDLSRLV 132
DB 57 ICRVPS---HKGMFSEFEDVLGMAVSFEQACPSLKIEYAFRIYDENENGFIDEEDLQRII 113
QY 133 NCLTGEDETRLSASEMKQIDNILEEXXXXXXXXXXXXXXOIVSRSPDPASSF 187
DB 114 LRLNLSDD---MSEDLMLDITNHVLSXSDLDNDNMLSEFEFHAKAKSPDEFWTFP 165

RESULT 9
US-09-802-116-2
; Sequence 2, Application US/09802116
; Patent No. US20020082406A1
; GENERAL INFORMATION:
; APPLICANT: Mathur, Brian
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. US20020082406A1el Human Kinase Interacting Protein and Polyn
; FILE REFERENCE: LEX-0146-USA
; CURRENT APPLICATION NUMBER: US/09/802,116
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 60/187,719
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 187
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-802-116-2

Query Match 35.8%; Score 324; DB 9; Length 187;
Best Local Similarity 37.3%; Pred. No. 1.6e-23;

Matches 72; Conservative 52; Mismatches 57; Indels 12; Gaps 5;
QY 1 MCGSGSRSLKELAEYODITLTKOEILLAHRRFCCELLPO---EORTVESSLRAQVPE 56
DB 1 MGNKQTVFTHEQLEAVQDDCTFTFRKREIMLFYRQDIALQVPLDYTTCPD---VKVPE 57
QY 57 OILSLPELKANPFKERICRVFSTSPAKDSLSFEDELILSVSDTAPDIKSHAFRIED 116
DB 58 LIGSMPELKDNPFRORIAOVES-EDDGHMTLDNFIDMFSVSEMAPRDLKAVYAFRIYD 116
QY 117 FDDDGTLNREDLSRLVNCITGEGEDTRLSASEMKQIDNILEEXXXXXXXXXXXXXXOIV 176
DB 117 FNNDDYICAMDEQYVTKTL-RGE---LSAEVSLVCAYLDEADGDHGRSLSEDFQNM 172
QY 177 ICRSPDPASSFKI 189
DB 173 ILRAPDFLSTFHI 185

RESULT 10
US-10-109-885-3
; Sequence 3, Application US/10109885
; Publication No. US20020119129A1
; GENERAL INFORMATION:
; APPLICANT: REVEL, Michel
; APPLICANT: CHERBATH, Judith
; APPLICANT: ABRAMOVIYCH, Carolina
; TITLE OF INVENTION: NOVEL IFN RECEPTOR I BINDING PROTEIN, DNA ENCODING THEM, AND M
; FILE REFERENCE: REVEL-14A
; CURRENT APPLICATION NUMBER: US/10/109,885
; PRIOR FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US/09/341,640
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: PCT/US98/00671
; PRIOR FILING DATE: 1998-01-15
; PRIOR APPLICATION NUMBER: US 60/035,636
; PRIOR FILING DATE: 1997-01-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentln version 3.1
; SEQ ID NO 3
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-109-885-3

Query Match 18.3%; Score 165.5; DB 14; Length 170;
Best Local Similarity 25.4%; Pred. No. 6e-08;
Matches 31; Conservative 44; Mismatches 42; Indels 5; Gaps 2;
QY 56 EOLSLPELKANPFKERICRVFSTSPAKDSLSFEDELILSVSDTAPDIKSHAFRIE 115
DB 41 EEFMSLPQLQNPQVORIVIDIFDTP-GNCEVDFKFEIEGVSPFKGDKCKLRAFRRIY 99
QY 116 FDDDGTLNREDLSRLVNCITGEGEDTRLSASEMKQIDNILEEXXXXXXXXXXXXXXOIV 175
DB 100 DMDKDGYSINGELFQVILKMWG-----NNLKDTQLQOIYDKTIINADKDDGRISFEFCA 155
QY 176 VI 177
DB 156 VV 157

RESULT 11
US-09-999-602-3
; Sequence 3, Application US/09999602
; Patent No. US20020091084A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti G.
; APPLICANT: Corley, Neil C.
; APPLICANT: Tang, Y. Tom

```

Query Match          17.3%  Score 157;  DB 9;  Length 214;
Best Local Similarity 24.4%;  Pred. No. 6.3e-07;
Matches      52;  Conservative      44;  Mismatches      69;  Indels      48;  Gaps      9;

QY      1  MGGSGSRLLSKELLAEYODLFETLKOEILLAHRRFCCELLPOEQRVTESLLRAQVPFEQLLS 60
DB      1  MGAHNS--ASEEVRLEBKRTGESSDQILQIHRRF--KQLSGDQPIIRK-----ENFNN 49
QY      61  LPELNAKFEKRICRVF-----STSPANDSIFEDFLDLVSYS--DTATPD----- 105
DB      50  VPDLLELNFIRSKIVRAFFDNRNLRKGPGLADEINFEFLVIMSTRFIDITTMDEQVEL 109
QY      106  ---IKSHAFRIPEPDDDDGTINREDLSRV--NCLTG---EGEDTR----- 143
DB      110  SRKKRLRFLFMYDSDSGRITLEEYRVNVEELLGNPHIKESARSIAQGMMEASVC 169
QY      144  LSASEMKOLIDNILEEXXXXXXXXXXXXXXOHV 176
DB      170  MGOHPDQVYEGITFEDEFLLKIMQIDIEITKMHV 202

RESULT 14
US-10-106-698-6128
: Sequence 6128, Application US/10106698
: Publication NO. US20030109690A1
GENERAL INFORMATION:
: APPLICANT: Ruben et al.
: TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypept
: FILE REFERENCE: P8005P1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR FILING DATE: 1999-11-03

```

```

; NUMBER OF SEQ ID NOS : 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 6128
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-106-698-6128

```

```

Query Match      17.3%; Score 157; DB 15; Length 257;
Best Local Similarity 24.4%; Pred. No. 8.8e-07;
Matches 52; Conservative 44; Mismatches 69; Indels 48; Gaps 9;

```

```

QY      1 MCGSGSRLSKELLAEYODLFLTKOEILLAHRRFCCLPQEOQTVESSLRAQVPEQILS 60
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      44 MGAHNS--ASEYVRELEGKTGSSDOIEQLHRRF--KQLSGDQPTIRK-----ENFNN 92
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      61 LPELKNPPEKRICRVF-----STSPAKDSLSEDFLDLLSVFS--DTATPD----- 105
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      93 VPDLEINPIRSKIVRAFPDNRMLRKGPSGLADEINDEFITMSYFRPIDTMDDEQVEL 152
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      106 ---IKSHVAFRIEDPDDDGTINREDLSRLV--NCLTG---EGEDTR----- 143
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      153 SRKEKRLFLFHMYSDDSGRTILEEYRNVEELLGPNHIEKESRSIADGAMERASVC 212
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      144 LSASEMKOLIDNILEEXXXXXXXXHOV 176
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      213 MCGMEPDQVEEGITFEEDFLKINQIDIEIKMHV 245
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 15

```

US-09-764-891-3897
; Sequence 3897, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3897
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-891-3897

```

```

Query Match      16.8%; Score 152; DB 11; Length 189;
Best Local Similarity 24.7%; Pred. No. 1.6e-06;
Matches 41; Conservative 44; Mismatches 65; Indels 16; Gaps 4;

```

```

QY      26 EILLAHRRFCCLPQEOQTVESSLRAQVPEQILSLPELKNPPEKRICRVESTSPAKDS 85
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      38 EIKRLGRRF-----KKLDLDKSGSLVEEEMSLPELRHNPVLRVIDVFDTD--GDGE 88
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      86 LSPEDFLDLSVFSDDTATPDIKSHVAFRIEDPDDDGTINREDLSRLVNCITGGEPTRLS 145
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      89 VDKKEITLTSGQSVKGDDEQKLRFAFSIYDMKDQGISNGELEQVLRKMWG---NNLT 144
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      146 ASEMKOLIDNILEEXXXXXXXXHOVISRSPDFASSFKIVL 191
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      145 DMQLQQLVDKTIITLIDKDGDKISFEFSAVVR---DLEIKKLV 187
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

Search completed: July 24, 2003, 13:23:01
 Job time : 24 secs

GenCore version 5.1.6
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OW protein - protein search, using sw model

Run on: July 24, 2003, 12:55:52 ; Search time 39 Seconds

(without alignments)
470.980 Million cell updates/sec

Title: SEQ2_MOD

Perfect score: 905

Sequence: 1 MGGSGSRSLSKELLAEYODLT.....XXQHVISRSPDFASSFKIVL 191

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	385	42.5	311	2	T21563
2	185.5	20.5	174	2	T41632
3	184.5	20.4	175	2	JH0462
4	169.5	18.7	174	2	T47245
5	167.5	18.5	369	2	T22708
6	165.5	18.3	170	1	A33391
7	165.5	18.3	170	1	S34127
8	165.5	18.3	170	1	JC11220
9	165.5	18.3	216	1	S42716
10	156	17.2	190	2	T20725
11	155.5	17.2	170	2	JC11221
12	154.5	17.1	170	2	JC11221
13	153.5	17.0	226	2	T51357
14	152.5	16.9	165	2	PS0261
15	152.5	16.9	170	2	JC7242
16	152.5	16.9	176	2	J01232
17	151.5	16.7	170	2	A44307
18	145.5	16.1	213	2	T31775
19	141.5	15.6	226	2	T08923
20	140.5	15.5	190	2	T51686
21	140.5	15.5	193	2	T28047
22	136.5	15.1	193	2	JH0816
23	136.5	15.1	193	2	T50676
24	135.5	15.0	193	2	S47565
25	135.5	15.0	213	2	T51356
26	132.5	14.6	190	2	A55666
27	132	14.6	246	2	T05308
28	132	14.6	246	2	H85387
29	131	14.5	192	2	T01375

30	129.5	14.3	193	2	JC2186
31	128.5	14.2	202	2	S21155
32	127.5	14.1	254	2	T29566
33	126	13.9	224	2	F96668
34	125	13.8	202	2	A46129
35	124.5	13.8	195	2	JC1347
36	124.5	13.8	202	2	T10531
37	123	13.6	191	2	JH0815
38	122.5	13.5	270	2	JC7631
39	121.5	13.4	193	2	JH0615
40	119	13.1	191	2	JH0605
41	119	13.1	191	2	A48979
42	118.5	13.1	190	2	S61168
43	118	13.0	214	2	T08922
44	117	12.9	190	2	S58303
45	115	12.7	756	2	C64236

ALIGNMENTS

RESULT 1
T21563
hypothetical protein F30A10.1 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C/Accession: T21563
R:Barlow, K.
submitted to the EMBL Data Library, October 1996
A/Reference number: Z19442
A/Accession: T21563
A/Status: preliminary; translated from GB/EMBL/DBDJ
A/Molecule type: DNA
A/Residues: 1-311 <Wtl>
A/Cross-references: EMBL:281072; PIDN:CA03019.1; GSPDB:GN00019; CESP:F30A10.1
A/Experimental source: Clone F30A10
A/Gene: CESP:F30A10.1
A/Map position: 1
A/Introns: 106/2; 139/3; 190/3; 240/1

Query Match
Best Local Similarity 39.1%; Score 385; DB 2; Length 311;
Matches 81; Conservative 51; Mismatches 49; Indels 26; Gaps 5;

QY 1 MGGSGSRSLSKELLAEYODLTFLKQETLLAHRRCCELLPOEQRTVESS 48
DB 111 MGNNASSUSELNFESKGGVFTREODEYODCTFFTRKDIIRLYKRFYALNPKH---VPTN 167
QY 49 LRAQVP-----FEQILSLPELKNPKPERICRVSTSPAKNSLSEDFDLDSVFSOTA 102
DB 168 MGNRPATITLTFEEVEKMPLEKNEPFRICEVS-EDGRNLSFDFLDFSVSEMA 226
QY 103 TPDIKSHVAFRIPEDDGTINREDLSRLVNCLEGEEDTRLSASEMKOLINILEEXXX 162
DB 227 PLQKTKYAFRIYDGDGLGHDLMSINSLTND-----ELSDVEVEFIIRITEADL 282
QY 163 XXXXXXXXXXXXQHVISRSPDFASSFKI 189
DB 283 GGDSSINFEEFEHVSRSDFIRTFHI 309

RESULT 2

T41632
probable calcineurin b subunit - fission yeast (Schizosaccharomyces pombe)
C/Species: Schizosaccharomyces pombe
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 04-Feb-2000
C/Accession: T41632
R:McDonnell, R.M.; Rajandream, M.A.; Barrell, B.G.; Ransperger, U.; Pohl, T.
submitted to the EMBL Data Library, August 1999
A/Reference number: Z22005
A/Accession: T41632
A/Status: preliminary; translated from GB/EMBL/DBDJ

C: Superfamily: calmodulin; calmodulin repeat homology
C: Keywords: blocked amino end; calcium binding; duplication; EF hand; heterodimer; 1
F: 2-170/Product: calcineurin regulatory chain; status predicted <MAT>
F: 18-49/Domain: calmodulin repeat homology <EF1>
F: 50-82/Domain: calmodulin repeat homology <EF2>
F: 87-119/Domain: calmodulin repeat homology <EF3>
F: 128-160/Domain: calmodulin repeat homology <EF4>
F: 2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F: 31/3/Modified site: aspartic acid (Asn) #status predicted
F: 63, 65, 67, 69, 74/Binding site: calcium (Asp, Asp, Ser, Ser, Glu) #status predicted
F: 100, 102, 104, 106, 111/Binding site: calcium (Asp, Asp, Asn, Glu, Glu) #status predicted
F: 141, 143, 145, 147, 152/Binding site: calcium (Asp, Asp, Asp, Tyr, Glu) #status predicted

Query Match 18.3% Score 165.5; DB 1; Length 170;
Best Local Similarity 25.4%; Pred. No. 9.2e-05;
Matches 31; Mismatches 42; Indels 5; Gaps 2;

QY 56 EQLSPELKNPKEKICRFSTSPAKDSFEDELFLSLSTPATPDIKSHYAFRI 115
D 41 EEFSLPELQGNPLVQNRVIDFPDD-GKGEVDKFEFTIGVQSFVSGKGEOKLRFAFRY 99
QY 116 DFDDGFLNREDLSRLVNCITGEGEDPRLSASEMKQOLIDNILEXXXXXXXQOH 175
D 100 DMDKDGYSINCELFQVLRKMGV---NNLKDTQLQQLIDKTIINADKDGGRISFEERCA 155
QY 176 VI 177
D 156 VV 157

RESULT 7
S34127
calcineurin regulatory chain [validated] - bovine
M: Alternate names: calcineurin beta subunit; calcineurin chain B; phosphoprotein phosphatase
C: Species: Bos primigenius taurus (cattle)
C: Date: 31-Dec-1993 #sequence revision 11-Dec-1993 #text_change 15-Sep-2000
C: Accession: I45831; J0297; S34127
R: Margang, C.E.; Bottrorf, D.A.; Adachi, K.
DNA Seq. 4, 313-318, 1994
A: Title: Isolation and characterization of a cDNA clone coding for the calcium-binding protein
A: Reference number: I45831; M01D:95102111; PMID:7803816
A: Accession: I45831
A: Status: preliminary; translated from GB/EMBL/DBJ
A: Molecule type: mRNA
A: Residues: 1170 <NA2>
A: Cross-references: EMBL:X71666; NID:9312968; PIDN:CA50659.1; PID:9312969
R: Attkin, A.; Klee, C.B.; Cohen, P.
Eur. J. Biochem. 139, 663-671, 1984
A: Title: The structure of the B subunit of calcineurin.
A: Reference number: J0297; M01D:84132092; PMID:6321184
A: Accession: J0297
A: Molecule type: protein
A: Residues: 211, 'M', 13-153, 'S', 155-169 <AT>
R: Griffith, J.P.; Kim, J.L.; Kim, E.E.; Sincchak, M.D.; Fitzgibbon, M.
Submitted to the Brookhaven Protein Data Bank, August 1996
A: Reference number: A66708; PDB:ITCO
R: Griffith, J.P.; Kim, J.L.; Kim, E.E.; Sincchak, M.D.; Thomson, J.A.; Fitzgibbon, M.
Cell 82, 507-522, 1995
A: Title: X-ray structure of calcineurin inhibited by the immunophilin-immunosuppressant cyclosporin A.
A: Reference number: A56967; M01D:95360994; PMID:7543369
A: Contents: annotation: X-ray crystallography, 2.5 angstroms
C: Complex: heterodimer with calcineurin catalytic chain (see PIR:A56968)
C: Superfamily: calmodulin; calmodulin repeat homology
C: Keywords: blocked amino end; calcium binding; duplication; EF hand; heterodimer; 1
F: 2-170/Product: calcineurin regulatory chain; status experimental <MAT>
F: 18-49/Domain: calmodulin repeat homology <EF1>
F: 50-82/Domain: calmodulin repeat homology <EF2>
F: 87-119/Domain: calmodulin repeat homology <EF3>
F: 128-160/Domain: calmodulin repeat homology <EF4>
F: 2/Modified site: myristylated amino end (Gly) (in mature form) #status experimental
F: 31/3/Modified site: aspartic acid (Asn) #status predicted

Db 138 FIERQEVKQVVATLAE-SGMNLIKDTVEDIIDKTFEEADTKHDKRIDKEWRSLVLRHP 196
QY 182 DFASSPKI 189
Db 197 SLIKNMTL 204

RESULT 14

PS0261
calciotaurin regulatory chain-like protein, testis - rat (fragment)
N:Alternate names: calciotaurin beta subunit; calciotaurin chain B; phosphoprotein phosphatase
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 13-Aug-1999
R:Accession: PS0261
R:Suppl. M.: Matsui, H.; Etch, S.; Shimizu, T.; Nishio, H.; Mota, L.J.M.P.; Tokuda, M.
B:Biochem. Biophys. Res. Commun. 189: 1476-1482, 1991
A:Title: Isolation and sequence of rat testis cDNA for a calcium binding polypeptide sim
A:Reference number: PS0261; MUID:92062183; PMID:1659420
A:Accession: PS0261
A:Molecule type: mRNA
A:Residues: 1-165 <SUG>
A:Cross-references: GB:S63991; NID:9238643; PIDN:AA820281.1; PID:9238644
C:Superfamily: calmodulin; calmodulin repeat homology
C:Keywords: blocked amino end; calcium binding; duplication; EF hand
F:7-38/Domain: calmodulin repeat homology <EF1>
F:39-71/Domain: calmodulin repeat homology <EF2>
F:76-108/Domain: calmodulin repeat homology <EF3>
F:117-149/Domain: calmodulin repeat homology <EF4>

Query Match

Best Local Similarity 16.9%; Score 152.5; DB 2; Length 165;
Matches 31; Conservative 41; Mismatches 45; Indels 5; Gaps 2;

QY 56 EDILSLPEIKANPFERICRVSTSPAKDSLSEDFDLDSVSDTPDPDKSHYAFRI 115
Db 30 DEFMSLPQLQNPVLRVIDIFPTD-GNGEVDFREFIVGTSQFSVKGDEQKLRFAFR 88
QY 116 DDDGGTINREDLSLVNLTGEGEDTRLSASEMKQIDNILEEXXXXXXXXHXH 175
Db 89 DMDNGFSTNGELFVLRKMGV-----NNLKMDQLQOLVDKSLVLRKDGDRISFEFRD 144

QY 176 VI 177
Db 145 VV 146

RESULT 15

JC7242

calciotaurin regulatory subunit, calciotaurin B - scallop (Palliopecten yessoensis)

N:Alternate names: Ca2+/calmodulin-dependent phosphoprotein phosphatase regulatory subunit

C:Species: Palliopecten yessoensis (Yesso scallop)

C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 21-Jul-2000

C:Accession: JC7242; PC7070

R:Uryu, M.; Nakatani, A.; Watanabe, M.; Hattuse, R.; Yazawa, M.

J. Biochem. 127: 739-746, 2000

A:Title: Molecular cloning of cDNA encoding two subunits of calciotaurin from scallop tes

A:Reference number: JC7241

A:Accession: JC7242

A:Molecule type: mRNA

A:Residues: 1-170 <URY>

A:Cross-references: DDBJ:AB041524

A:Experimental source: testis

A:Accession: PC7070

A:Molecule type: Protein

A:Residues: 12-68;73-85;92-170 <UR2>

C:Comment: This protein, one of Ca2+/calmodulin-dependent enzyme, is a testis-specific

C:Genetics:

A:Gene: cnb

C:Superfamily: calmodulin; calmodulin repeat homology

C:Keywords: calcium binding; EF hand; flagellar rotation; myristylation; phosphoprotein;

Best Local Similarity 21.1%; Pred. No. 0 00082;
Matches 37; Conservative 53; Mismatches 66; Indels 19; Gaps 4;

QY 3 GSGSLRSLKEALLAEYODTLTKOELLNHRRCCELLPOEQRVSSIRAAVPEQILSLP 62
Db 2 GNENSLPMELCSNFD-----PDEIKRLGRF-----RKLDLNSGSLSDVDMTLP 47
QY 63 ELKANPFERICRVSTSPAKDSLSEDFDLDSVSDTPDPDKSHYAFRI 122
Db 48 ELQONPLVQRVIDIFPTD-GNGEVDFREFIVGTSQFSVKGDKLRLFAFRKIYDMKDG 106
QY 123 LNREDLSRLVNCUTGEGEDTRLSASEMKQIDNILEEXXXXXXXXHXH 177
Db 107 ISNGELFVLRKMGV-----NNLKMDQLQOLVDKSLVLRKDGDRISFEFRD 157

Search completed: July 24, 2003, 13:19:24
Job time : 44 secs

Query Match 16.9%; Score 152.5; DB 2; Length 170;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 24, 2003, 12:55:51 ; Search time 23 Seconds

(without alignments)
390.526 Million cell updates/sec

Title: SEQ2_MOD

Sequence: 1 MGGSGSRLSKELAEYQDLT.....XXQHYISRPFFASSFKIVL 191

Scoring table: BLOSUM62DX

Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	905	100.0	191	KIP1_HUMAN	Q99828 homo sapien
2	852	94.1	191	KIP1_MOUSE	Q940f4 mus musculu
3	851	94.0	191	KIP1_RAT	Q94010 rattus norv
4	324	35.8	187	KIP2_MOUSE	Q94309 mus musculu
5	322	35.6	187	KIP2_HUMAN	O78838 homo sapien
6	195.5	21.6	177	CALB_NABGR	P43322 naegleria g
7	185.5	20.5	174	CALB_SCHPO	Q9nu93 schizosacch
8	179.5	19.8	174	CALB_YEAST	P25296 saccharomyc
9	169.5	18.7	174	CALB_NEUCR	P87072 neurospora
10	165.5	18.3	169	CALB_HUMAN	P06705 homo sapien
11	165.5	18.3	169	CALB_MOUSE	O63810 mus musculu
12	161	17.8	194	CA22_MOUSE	Q96bs2 mus musculu
13	157	17.3	214	CA22_MOUSE	O63877 mus musculu
14	156	17.2	189	TESC_HUMAN	P36609 caenorhabdi
15	156	17.2	194	CA22_MOUSE	O99653 homo sapien
16	155.5	17.2	170	CALC_DROME	O24214 drosophila
17	154.5	17.1	178	CALC_DROME	O63811 mus musculu
18	154.5	17.1	186	APLC_MOUSE	P37236 drosophila
19	154.5	17.1	190	APLC_MOUSE	P46981 aplysia cal
20	151.5	16.9	175	CALC_RAT	P28470 rattus norv
21	151.5	16.7	170	CALB_DROME	P48451 drosophila
22	150	16.6	214	TESC_MOUSE	O91k15 mus musculu
23	135.5	15.0	189	NCSI_HUMAN	P36610 homo sapien
24	135.5	15.0	189	NCSI_MOUSE	Q91614 xenopus lae
25	135	14.9	190	NCSI_XENLA	P36608 caenorhabdi
26	133.5	14.8	195	NCSI_MOUSE	O43745 homo sapien
27	131.5	14.5	192	VIS3_CHICK	P42324 gallus gall
28	131.5	14.5	192	VIS3_MOUSE	P53333 mus musculu
29	130.5	14.4	192	VIS3_HUMAN	P37235 homo sapien
30	127.5	14.1	189	NCAH_DROME	P23235 drosophila
31	124.5	13.8	192	HIPP_HUMAN	P22076 homo sapien
32	123.5	13.6	201	RECO_MOUSE	P34057 mus musculu
33	122.5	13.5	201	SMOD_RANCA	P31227 rana catesb

34	120.5	13.3	192	NECX_APLCA	Q16962 aplysia cal
35	120	13.3	201	RECO_BOVIN	P21457 bos taurus
36	118	13.0	190	VIS2_RAT	P35332 rattus norv
37	117.5	13.0	192	NCAH_CHICK	O12953 gallus gall
38	116.5	12.9	192	NCAH_HUMAN	P29542 gallus gall
39	116.5	12.9	192	NCAH_MOUSE	O91x57 mus musculu
40	115	12.7	756	Y328_MYGE	Q49419 mycoplasma
41	114	12.6	190	VIS1_HUMAN	P28677 homo sapien
42	113.5	12.5	189	NCSI_MOUSE	O06389 saccharomyc
43	112	12.4	189	NCSI_SCHPO	O09711 schizosacch
44	110.5	12.2	158	TPCI_BALNU	P21787 balanus nub
45	109.5	12.1	172	CET1_MOUSE	P41209 mus musculu

ALIGNMENTS

RESULT 1

KIP1_HUMAN STANDARD; PRT; 191 AA.
AC Q99828; O00693; O00735; Q96J54; Q99971;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Calcium and integrin-binding protein 1 (Calmyrin) (DNA-PKcs
DE Interacting protein) (Kinase interacting protein) (KIP) (SNK
DE CIB1 OR PRKDCIP OR KIP OR CIB.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Yuan O.;
RT "SNK, a Ser/Thr protein kinase, associated proteins.";
RL Submitted (JAN-1997). to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE-98040126; PubMed-9372844;
RX MEDLINE-97184102; PubMed-9030514;
RC TISSUE=Fetal liver;
RT "Interaction between DNA-dependent protein kinase and a novel protein,
RT KIP.";
RL Mutat. Res. 385:13-20(1997).
RN [3]
RP SEQUENCE FROM N.A.
RA MEDLINE-97184102; PubMed-9030514;
RX "Identification of a novel calcium-binding protein that interacts
RT with the integrin alpha1b cytoplasmic domain.";
RL J. Biol. Chem. 272:4651-4654(1997).
RN [4]
RP SEQUENCE FROM N.A.
RA MEDLINE-20284952; PubMed-10826701;
RX Hattori A., Seki N., Hayashi A., Kozuma S., Saito T.;
RT "Genomic structure of mouse and human genes for DNA-PKcs interacting
RT protein (KIP).";
RL DNA Seq. 10:415-418(2000).
RN [5]
RP SEQUENCE FROM N.A.
RA TISSUE=Cervix;
RX MEDLINE-22388257; PubMed-12477932;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshlyuk S., Carninci P., Prange C.,
RA Bosa S., Loguigliano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Holyk S.W.,

RA Villalón D.R., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
 RA Butlerfield Y.S.N., Krzyzinski M.I., Skalska U., Smalilus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6]
 RP STRUCTURE BY NMR OF 9-191.
 RX MEDLINE-20283154; PubMed-10822252;
 RA Hwang P.M., Vogel H.J.;
 RT "Structures of the platelet calcium- and integrin-binding protein and
 RT the alphaIIb-integrin cytoplasmic domain suggest a mechanism for
 RT calcium-regulated recognition, homology modelling and NMR studies.";
 RL J. Mol. Recognit. 13:83-92(2000).
 CC -1- FUNCTION: MAY CONVERT THE INACTIVE CONFORMATION OF INTEGRIN ALPHA-
 CC IIB/BETA3 TO AN ACTIVE FORM THROUGH THE BINDING TO THE INTEGRIN
 CC CYTOPLASMIC DOMAIN.
 CC -1- SUBUNIT: INTERACTS WITH THE HETERODIMERIC INTEGRIN ALPHA-
 CC IIB/BETA3. INTERACTS WITH THE PROTEIN KINASES SRK AND WITH THE
 CC REGION IMMEDIATELY UPSTREAM OF THE KINASE DOMAIN OF DNA-PK.
 CC -1- TISSUE SPECIFICITY: Ubiquitous.
 CC -1- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
 CC -----
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 CC -----
 DR EMBL: U08236; AAB39758.1; -
 DR EMBL: U08561; AAB5387.1; -
 DR EMBL: U08226; AAC5106.1; -
 DR EMBL: AB021866; BAA36281.1; -
 DR EMBL: BC000846; AAR00846.1; -
 DR PDB: 1DGV; 08-DEC-99.
 DR PDB: 1DGV; 30-AUG-00.
 DR Genew; HSCN:16920; CIB1.
 DR MM; 602293; -
 DR GO: GO:0005515; F:protein binding activity; TAS.
 DR GO: GO:0007155; P:cell adhesion; TAS.
 DR GO: GO:0006302; P:double-strand break repair; TAS.
 DR InterPro: IPR002048; EF-hand.
 DR Pfam: PF00036; efhand; 2.
 DR ProDom: PD000012; EF-hand; 1.
 DR SMART: SM00054; Efh; 2.
 DR PROSITE: PS00018; EF_HAND; 2.
 KM Calcium-binding; Repeat; 3d-structure.
 FT CA_BIND 116 127 EF-HAND 1 (POTENTIAL).
 FT CA_BIND 161 172 EF-HAND 2 (POTENTIAL).
 FT CONFICT 44 44 T -> S (IN REF. 3 AND 5).
 FT HELIX 24 37
 FT TURN 39 42
 FT TURN 49 51
 FT TURN 55 58
 FT HELIX 59 60
 FT TURN 62 63
 FT TURN 68 69
 FT TURN 70 77
 FT HELIX 78 78
 FT HELIX 88 98
 FT TURN 100 101
 FT HELIX 104 115
 FT STRAND 123 124
 FT HELIX 125 135
 FT TURN 136 140
 FT HELIX 143 159
 FT TURN 160 161

FT TURN 163 165
 FT STRAND 167 168
 FT HELIX 170 177
 FT TURN 178 179
 FT TURN 183 184
 SO SEQUENCE 191 AA; 21717 MW; 9AA6EA7897881E55 CRC64;
 Query Match 100.0%; Score 905; DB 1; Length 191;
 Best Local Similarity 92.7%; Pred. No. 1.2e-60;
 Matches 177; Conservative 14; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGSGSRLSKELLAEYODLFTFKOEILLAHRRCELLPOEORTVESSLRAOVFEQILS 60
 DB 1 MGSGSRLSKELLAEYODLFTFKOEILLAHRRCELLPOEORTVESSLRAOVFEQILS 60
 QY 61 LPELKNPFKERICRVFSTSPAKDSLSFEDFLDLVSFDPAPDIKSHYAFRIFFDD 120
 DB 61 LPELKNPFKERICRVFSTSPAKDSLSFEDFLDLVSFDPAPDIKSHYAFRIFFDD 120
 QY 121 GTLNREDLSRLVNCITGEGDTRLSASEMKQIDNILEEXXXXXXXOHTVSR 180
 DB 121 GTLNREDLSRLVNCITGEGDTRLSASEMKQIDNILEESDIDRDGTTNSEFOHVSRS 180
 QY 181 PDFASSEKIVL 191
 DB 181 PDFASSEKIVL 191
 DB 181 PDFASSEKIVL 191
 RESULT 2
 ID KIP1_MOUSE STANDARD; PRT; 191 AA.
 AC 0920F4;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Calcium and integrin-binding protein 1 (Calmyrin) (DNA-PKcs
 DE interacting protein) (Kinase interacting protein) (KIP) (CIB).
 GN CIB1 OR PRKDCIP OR KIP OR CIB.
 OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE-99069785; PubMed-9852683;
 RA Seki N., Hayashi A., Abe M., Araki R., Fujimori A., Fukumura R.,
 RA Hattori A., Kozuma S., Ohlira M., Hori T., Saito T.;
 RT "Chromosomal assignment of the gene for human DNA-PKcs interacting
 RT protein (KIP) on chromosome 15q25.3-q26.1 by somatic hybrid analysis
 RT and fluorescence in situ hybridization.";
 RL J. Hum. Genet. 43:275-277(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Fetal kidney;
 RX MEDLINE-99160477; PubMed-10051332;
 RA Saito T., Seki N., Hattori A., Hayashi A., Abe M., Araki R.,
 RA Fujimori A., Fukumura R., Kozuma S., Matsuda Y.;
 RT "Structure, expression profile, and chromosomal location of a mouse
 RT gene homologous to human DNA-PKcs interacting protein (KIP) gene.";
 RL Mamm. Genome 10:315-317(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Naik M.U., Naik U.P.;
 RT "Cloning and tissue distribution of murine calcium and integrin
 RT binding protein, CIB.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RX MEDLINE-21085660; PubMed-11217851;
 RA Kawai J., Shinagawa A., Shibata Y., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Alzava K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
 RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gasterland T., Gliss C., Kling B., Kochiwa H.,
 RA Knehl P., Lewis S., Matsuo Y., Nishida I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Bash G.,
 RA Blake J., Boileau D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher K., Fujita M., Gariboldi M.,
 RA Gustincich S., Hall D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilmshurst L.,
 RA Yuzhakov-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection."
 CC Nature 409:685-690(2001).
 CC -1- FUNCTION: MAY CONVERT THE INACTIVE CONFORMATION OF INTEGRIN ALPHA-
 CC IIB/BETA3 TO AN ACTIVE FORM THROUGH THE BINDING TO THE INTEGRIN
 CC CYTOPLASMIC DOMAIN (BY SIMILARITY).
 CC -1- SUBUNIT: INTERACTS WITH THE HETERODIMERIC INTEGRIN ALPHA-
 CC IIB/BETA3. INTERACTS WITH THE PROTEIN KINASES SNK AND WITH THE
 CC REGION IMMEDIATELY UPSTREAM OF THE KINASE DOMAIN OF DNA-PK (BY
 CC SIMILARITY).
 CC -1- TISSUE SPECIFICITY: Ubiquitous.
 CC -1- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
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 CC
 DR EMBL: AB006463; BAA74429.1;
 DR EMBL: AB017361; BAA36165.1;
 DR EMBL: AF173010; AAC38960.1;
 DR EMBL: AK010345; BAB26868.1;
 DR HSSP: Q99828; IDGV.
 DR MGD: MGI:1344418; Clb1.
 DR InterPro: IPR002048; EF-hand.
 DR Pfam: PF00036; ehand; 2.
 DR ProDom: PD000012; EF-hand; 1.
 DR SMART: SM00054; EFh; 2.
 DR PROSITE: PS00018; EF_HAND; 2.
 KW Calcium-binding; Repeat.
 KW CA_BIND 116 127 EF-HAND 1 (POTENTIAL).
 FT CA_BIND 161 172 EF-HAND 2 (POTENTIAL).
 FT SEQUENCE 191 AA; 21763 MW; C85B603A19F9D9AC.CRC64;
 SO
 Query Match 94.1%; Score 852; DB 1; Length 191;
 Best Local Similarity 86.9%; Pred. No. 1.1e-56;
 Matches 166; Conservative 18; Mismatches 7; Indels 0; Gaps 0;
 QY 1 MGSGSRLSKELLAEYODLFTLKOEITLARRCELLPOQRVSSLRQVPEQILS 60
 DB 1 MGSGSRLSKELLAEYODLFTLKOEITLARRCELLPPQRVSSLRQVPEQILS 60
 QY 61 LPELKANPFKERICRVSTSPKADSLSFEDFLDLVSFSDATPDIKSHAFRIFFPDD 120
 DB 61 LPELKANPFKERICRVSTSPKADSLSFEDFLDLVSFSDATPDIKSHAFRIFFPDD 120
 QY 121 GTLNREDLSLVNCLTGEEDTRLASSEMQLIDNILEEXXXXXXXXHOHVSRS 180
 DB 121 GTLNREDLSLVNCLTGEEDTRLASSEMQLIDNILEESIDRDGTINLSEFQHVISRS 180
 QY 181 PDFASSFKIVL 191
 DB 181 PDFASSFKIVL 191

RESULT 3
 ID KIP1_RAT STANDARD; PRT; 191 AA.
 AC KIP1_RAT
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Calcium and integrin-binding protein 1 (Calmyrin) (DNA-PKcs
 DE interacting protein) (kinase interacting protein) (KIP) (CIB).
 GN CIB1 OR PRKDCIP OR KIP OR CIB.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99452760; PubMed=10523297;
 RA Kauselmann G., Weiler M., Wolf P., Jessberger S., Konietzko U.,
 RA Scafidi J., Staudil U., Betsler-Hahn J., Streibhardt K., Kuhl D.;
 RT "The polo-like protein kinases Fnk and Snk associate with a Ca(2+)-and
 RT integrin-binding protein and are regulated dynamically with synaptic
 RT plasticity."
 RT EMBO J. 18:5528-5539(1999).
 CC -1- FUNCTION: MAY CONVERT THE INACTIVE CONFORMATION OF INTEGRIN ALPHA-
 CC IIB/BETA3 TO AN ACTIVE FORM THROUGH THE BINDING TO THE INTEGRIN
 CC CYTOPLASMIC DOMAIN (BY SIMILARITY).
 CC -1- SUBUNIT: INTERACTS WITH THE HETERODIMERIC INTEGRIN ALPHA-
 CC IIB/BETA3. INTERACTS WITH THE PROTEIN KINASES SNK AND WITH THE
 CC REGION IMMEDIATELY UPSTREAM OF THE KINASE DOMAIN OF DNA-PK (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
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 CC
 DR EMBL: AF136585; AAF08368.1;
 DR HSSP: Q99828; IDGV.
 DR InterPro: IPR002048; EF-hand.
 DR Pfam: PF00036; ehand; 2.
 DR ProDom: PD000012; EF-hand; 1.
 DR SMART: SM00054; EFh; 2.
 DR PROSITE: PS00018; EF_HAND; 2.
 KW Calcium-binding; Repeat.
 KW CA_BIND 116 127 EF-HAND 1 (POTENTIAL).
 FT CA_BIND 161 172 EF-HAND 2 (POTENTIAL).
 FT SEQUENCE 191 AA; 21800 MW; 3B00B028879PCC.CRC64;
 SO
 Query Match 94.0%; Score 851; DB 1; Length 191;
 Best Local Similarity 86.9%; Pred. No. 1.3e-56;
 Matches 166; Conservative 17; Mismatches 8; Indels 0; Gaps 0;
 QY 1 MGSGSRLSKELLAEYODLFTLKOEITLARRCELLPOQRVSSLRQVPEQILS 60
 DB 1 MGSGSRLSKELLAEYODLFTLKOEITLARRCELLPPQRVSSLRQVPEQILS 60
 QY 61 LPELKANPFKERICRVSTSPKADSLSFEDFLDLVSFSDATPDIKSHAFRIFFPDD 120
 DB 61 LPELKANPFKERICRVSTSPKADSLSFEDFLDLVSFSDATPDIKSHAFRIFFPDD 120
 QY 121 GTLNREDLSLVNCLTGEEDTRLASSEMQLIDNILEEXXXXXXXXHOHVSRS 180
 DB 121 GTLNREDLSLVNCLTGEEDTRLASSEMQLIDNILEESIDRDGTINLSEFQHVISRS 180
 QY 181 PDFASSFKIVL 191
 DB 181 PDFASSFKIVL 191

```

RESULT 4
KIP2_MOUSE
ID KIP2_MOUSE STANDARD: PRT: 167 AA.
AC Q92309:
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Kinase interacting protein 2 (KIP 2).
GN KIP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain, and Testis;
RX MEDLINE=99132027; PubMed=9931475;
RA Seki N., Hattori A., Hayashi A., Kozuma S., Ohira M., Hori T.,
RA Saito T.;
RT "Structure, expression profile and chromosomal location of an isolog
RT of DNA-PKcs interacting protein (KIP) gene.";
RL Blochim Biophys. Acta 1444:143-147(1999).
CC -1- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
CC .....
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CC .....
DR EMBL: AB016080; BAA36545.1;
DR HSP: Q99828; IDGV.
DR MGD: MGI:1929293; KIP2.
DR InterPro: IPR02048; EF-hand.
DR Pfam: PF00036; ehand; 3.
DR ProDom: PD000012; EF-hand; 1.
DR SMART: SM00054; EFN; 2.
DR PROSITE: PS00018; EF_HAND; 2.
KW Calcium-binding; Repeat.
FT CA_BIND 116 127 EF-HAND 1 (POTENTIAL).
FT CA_BIND 157 168 EF-HAND 2 (POTENTIAL).
SQ SEQUENCE 187 AA; 21703 MW; D21D21DCBD086F5C CRC64;

Query Match 35.88; Score 324; DB 1; Length 187;
Best Local Similarity 35.28; Pred. No. 3.7e-17;
Matches 68; Conservative 52; Mismatches 61; Indels 12; Gaps 4;

QY 1 MGSGSRSLKELAEYODLFTLKOEITLAHRRFCE---LLPOEQTVESLRAQVFE 56
DB 1 MGNKQITFTEBOLDNYDCCTFFNKKDILKHSREYELAPNLYPMDYR---KSPIVHWMS 57
QY 57 QILSLPELKNPFERKICRVSTSPAKDSLSEFEDLDLSVFSPTAPDIDKSHVAFRIFD 116
DB 58 LIIMPFLKRNPFERIVAEAFS-EDGEGLNLTFNDFVDFSVLCSPAPELAKANAFKIYD 116
QY 117 FDDDGTLNRDLSRLVNCCLTGEEDTRLASSEMQLDNLIEKXXXXXXXKXOHV 176
DB 117 FNTDNFTCKEDLETLARLT---KSELDEEYVLVCKVIEADLDGDKLGFADEDM 172
QY 177 ISRSPDFASSEFKI 189
DB 173 IAKAPDELSTFTHI 185

RESULT 5
KIP2_HUMAN
ID KIP2_HUMAN STANDARD: PRT: 167 AA.
AC Q75838:
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

```

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DE Kinase interacting protein 2 (KIP 2).
GN KIP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RX MEDLINE=99132027; PubMed=9931475;
RA Seki N., Hattori A., Hayashi A., Kozuma S., Ohira M., Hori T.,
RA Saito T.;
RT "Structure, expression profile and chromosomal location of an isolog
RT of DNA-PKcs interacting protein (KIP) gene.";
RL Blochim Biophys. Acta 1444:143-147(1999).
CC -1- TISSUE SPECIFICITY: Ubiquitous.
CC -1- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
CC .....
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CC .....
DR EMBL: AB012955; BAA33584.1;
DR HSP: Q99828; IDGV.
DR MIM: 605564;
DR GO: GO:0005515; F:protein binding activity; TAS.
DR InterPro: IPR02048; EF-hand.
DR Pfam: PF00036; ehand; 3.
DR ProDom: PD000012; EF-hand; 1.
DR SMART: SM00054; EFN; 2.
DR PROSITE: PS00018; EF_HAND; 2.
KW Calcium-binding; Repeat.
FT CA_BIND 116 127 EF-HAND 1 (POTENTIAL).
FT CA_BIND 157 168 EF-HAND 2 (POTENTIAL).
SQ SEQUENCE 187 AA; 21643 MW; D51FC25AD381BEF CRC64;

Query Match 35.68; Score 322; DB 1; Length 187;
Best Local Similarity 35.28; Pred. No. 5.3e-17;
Matches 68; Conservative 52; Mismatches 61; Indels 12; Gaps 4;

QY 1 MGSGSRSLKELAEYODLFTLKOEITLAHRRFCE---LLPOEQTVESLRAQVFE 56
DB 1 MGNKQITFTEBOLDNYDCCTFFNKKDILKHSREYELAPNLYPMDYR---KSPIVHWMS 57
QY 57 QILSLPELKNPFERKICRVSTSPAKDSLSEFEDLDLSVFSPTAPDIDKSHVAFRIFD 116
DB 58 LIIMPFLKRNPFERIVAEAFS-EDGEGLNLTFNDFVDFSVLCSPAPELAKANAFKIYD 116
QY 117 FDDDGTLNRDLSRLVNCCLTGEEDTRLASSEMQLDNLIEKXXXXXXXKXOHV 176
DB 117 FNTDNFTCKEDLETLARLT---KSELDEEYVLVCKVIEADLDGDKLGFADEDM 172
QY 177 ISRSPDFASSEFKI 189
DB 173 IAKAPDELSTFTHI 185

RESULT 6
CALB_NAEGR
ID CALB_NAEGR STANDARD: PRT: 177 AA.
AC P42322;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calcineurin B subunit (Protein phosphatase 2B regulatory subunit)
DE (Calcineurin regulatory subunit).
GN CMB1.
OS Neogleria gruberi.
OC Eukaryota; Heterobiosae; Schizopyrenidae; Vahlkampfiidae; Neogleria.

```


NCBI_TaxID=5762;
 OX [1]
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN-NEG;
 RX MEDLINE=95172399; PubMed=7867946;
 RA Remillard S.P., Lai E.Y., Levy Y.Y., Fulton C.;
 RT "A calcineurin-B-encoding gene expressed during differentiation of
 the amoebal flagellate Naegleria gruberi contains two introns."
 RL Gene 151:39-45(1995).
 CC
 -1- FUNCTION: REGULATORY SUBUNIT OF CALCINEURIN, A CALCIUM-DEPENDENT,
 CALMODULIN STIMULATED PROTEIN PHOSPHATASE. CONFERS CALCIUM
 SENSITIVITY (BY SIMILARITY).
 CC
 -1- SUBUNIT: COMPOSED OF A CATALYTIC SUBUNIT (A) AND A REGULATORY
 SUBUNIT (B) (BY SIMILARITY).
 CC
 -1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
 SITES (BY SIMILARITY).
 CC
 -1- SIMILARITY: Contains 4 EF-hand calcium-binding domains.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL: U04380; AA81896.1; -
 DR HSSP: P06705; IAU1.
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR001125; Recoverin.
 DR Pfam: PF00036; ehand; 4.
 DR PRINTS: PR00450; RECOVERIN.
 DR PRODOM: PD000012; EF-hand; 2.
 DR SMART: SM00054; EFh; 4.
 DR PROSITE: PS00018; EF-HAND; 4.
 DR Calcium-binding; Repeat.
 DR CA_BIND 38 49 EF-HAND 1 (BY SIMILARITY).
 DR FT 70 81 EF-HAND 2 (BY SIMILARITY).
 DR FT 107 118 EF-HAND 3 (BY SIMILARITY).
 DR CA_BIND 148 159 EF-HAND 4 (BY SIMILARITY).
 DR CA_BIND 177 AA; 20057 MW; 01D4A48E947E97C CRC64;
 SQ SEQUENCE
 Query Match 21.6%; Score 195.5; DB 1; Length 177;
 Best Local Similarity 25.3%; Pred. No. 1.5e-07;
 Matches 45; Conservative 52; Mismatches 68; Indels 13; Gaps 3;
 OY 1 MGSGSRSLKELAEYQDITFLTKOETLAHRRCELLPQEQRVESSLAQVPEOILS 60
 DB 1 MGMTSSLREVEVEEMKGTNFTOKETKLTNRKTKLDKNGTISK-----DEFLM 52
 OY 61 LPELKNPFKEKICRVFTSPSPADSFEEDFLDLVSFSDPATVPDIKSHYAFRIEDDD 120
 DB 53 IPELVNPLVKRIVISFDEN-GDGSVNEKEFIALSVFNAGKQKRLERAFVYDIDGD 111
 OY 121 GTNRDDLSRLVNCILGEGEDTFLSASEMKQILDNILEXXXXXXXHXHXYIS 178
 DB 112 GYISNELFTVLKAMVG-----NNLSQVQIQIVDKITILEADEDDGDKISPEEFARKLS 165
 RESULT 7
 ID CALB_SCHPO STANDARD; PRT; 174 AA.
 AC 09U93;
 DT 16-OCT-2001 (Rel. 40; Created)
 DT 16-OCT-2001 (Rel. 40; Last sequence update)
 DT 28-FEB-2003 (Rel. 41; Last annotation update)
 DE Calcineurin B subunit (protein phosphatase 2B regulatory subunit)
 DE (Calcineurin regulatory subunit).
 GN CNB1 OR SRC830.06.
 OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomyces.

NCBI_TaxID=4896;
 OX [1]
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN-972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Scouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murall M., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson S., Quay M.A., Rabinowitsch E.,
 RA Rutherford J., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Slimmons M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volkhardt G., Aert R., Robben J., Grymonprez B.,
 RA Welfens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lebrach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Medler H., Wambut R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaur V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomyces pombe".
 RL Nature 415:871-880(2002).
 CC
 -1- FUNCTION: REGULATORY SUBUNIT OF CALCINEURIN, A CALCIUM-DEPENDENT,
 CALMODULIN STIMULATED PROTEIN PHOSPHATASE. CONFERS CALCIUM
 SENSITIVITY (BY SIMILARITY).
 CC
 -1- SUBUNIT: COMPOSED OF A CATALYTIC SUBUNIT (A) AND A REGULATORY
 SUBUNIT (B) (BY SIMILARITY).
 CC
 -1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
 SITES (BY SIMILARITY).
 CC
 -1- SIMILARITY: Contains 4 EF-hand calcium-binding domains.
 CC
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 CC
 DR EMBL: AL109850; CAB52879.1; -
 DR PIR: T41632; T41632.
 DR HSSP: P06705; IAU1.
 DR GeneDB_Spombe: SPCC830.06; -
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR001125; Recoverin.
 DR Pfam: PF00036; ehand; 4.
 DR PRINTS: PR00450; RECOVERIN.
 DR PRODOM: PD000012; EF-hand; 1.
 DR SMART: SM00054; EFh; 4.
 DR PROSITE: PS00018; EF-HAND; 4.
 DR Calcium-binding; Myristate.
 DR CA_BIND 34 45 EF-HAND 1 (BY SIMILARITY).
 DR FT 66 77 EF-HAND 2 (BY SIMILARITY).
 DR CA_BIND 103 114 EF-HAND 3 (BY SIMILARITY).
 DR FT 144 155 EF-HAND 4 (BY SIMILARITY).
 DR CA_BIND 174 AA; 19675 MW; EEF38FE4959442E CRC64;
 SQ SEQUENCE
 Query Match 20.5%; Score 185.5; DB 1; Length 174;
 Best Local Similarity 22.8%; Pred. No. 8e-07;
 Matches 41; Conservative 59; Mismatches 63; Indels 17; Gaps 4;
 OY 1 MGSGSRSLKELAEYQDITFLTKOETLAHRRCELLPQEQRVESSLAQVPEOILS 60
 DB 1 MGSOSQIFEDLISN-----SFSNEIERIRIRRFIK-----IDANGSIDRNEFLS 48

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QY 61 LPELKANPFRKICRVFSTSPAKDSLSFEFDLLSVFSDTATPDIKSHYAFRIFDDDD 120
DB 49 IPVSASNPPLASRLFSVYDEGGD-VDFQEFINSLSFVHGKKEELKRAFKYIDDD 107
QY 121 GTLNREDLSRLVNCITGEGEDTRLASASEMKOLIDNILEXXXXXXXQXQHVIRS 180
DB 108 GYISNGELIYLVKMWG-----TJLNREDLOQIVDKRTIMEVDKDRGKISFEEDIVSGS 163

RESULT 8
CALB_YEAST STANDARD; PRT; 174 AA.
ID CALB_YEAST STANDARD; PRT; 174 AA.
AC P25296;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calcineurin B subunit (Protein phosphatase 2B regulatory subunit)
GN CNB1 OR YCNB OR YCN2 OR YKL190M.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A364A.
RX MEDLINE=92062059; PubMed=1659397;
RA Kuno T., Tanaka H., Mukai H., Chang C.-D., Hiraga K., Miyakawa T.,
RA Tanaka C.;
RT "cDNA cloning of a calcineurin B homolog in Saccharomyces
RT cerevisiae."
RL Biochem. Biophys. Res. Commun. 180:1159-1163(1991).
RN [2]
RP SEQUENCE FROM N.A. AND MYRISTOLATION.
RX MEDLINE=92334345; PubMed=1321337;
RA Cyert M.S., Thorner J.;
RT "Regulatory subunit (CNB1 gene product) of yeast Ca2+/calmodulin-
RT dependent phosphoprotein phosphatases is required for adaptation to
RT pheromone."
RL Mol. Cell. Biol. 12:3460-3469(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=GRF88;
RX MEDLINE=93348778; PubMed=8394042;
RA Cheret G., Matheakis L.C., Sor F.;
RT "DNA sequence analysis of the YCN2 region of chromosome XI in
RT Saccharomyces cerevisiae."
RL Yeast 9:661-667(1993).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=94205264; PubMed=8154185;
RA Wiemann S., Voss H., Schwager C., Rupp T., Stegemann J.,
RA Zimmermann J., Grochues D., Sensen C., Erfle H., Hewitt N.,
RA Banerji A., Ansoorge W.;
RT "Sequencing and analysis of 51.6 kilobases on the left arm of
RT chromosome XI from Saccharomyces cerevisiae reveals 23 open reading
RT frames including the FAS1 gene."
RL Yeast 9:1343-1348(1993).
RN [5]
RP SEQUENCE FROM N.A.
RA Mala e Silva A., Bossier P., Vilela C., Fernandes L., Soares H.,
RA Guerreiro P., Rodrigues-Pousada C.;
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: REGULATORY SUBUNIT OF CALCINEURIN, A CALCIUM-DEPENDENT,
CC CALMODULIN STIMULATED PROTEIN PHOSPHATASE. CONFERS CALCIUM
CC SENSITIVITY.
CC -1- SUBUNIT: COMPOSED OF A CATALYTIC SUBUNIT (A) AND A REGULATORY
CC SUBUNIT (B).
CC -1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
CC SITES.
CC -1- SIMILARITY: Contains 4 EF-hand calcium-binding domains.

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CC -----
DR EMBL: Z26521; CA81290.1; -
DR EMBL: D10293; BAA01136.1; -
DR EMBL: M87508; AAA34505.1; -
DR EMBL: X69765; CAA49421.1; -
DR EMBL: X74151; CAA52248.1; ALT_INIT.
DR EMBL: Z28190; CAA82034.1; -
DR EMBL: Z28189; CAA82033.1; -
DR PIR: JH0462; JH0462.
DR HSSP: P06705; IAO1.
DR SCD: S0001673; CNB1.
DR GO: GO:0004723; F:calcium-dependent protein serine/threonine . . . IPI.
DR GO: GO:0000754; P:adaptation to pheromone during conjugation . . . IMP.
DR GO: GO:0006873; P:cell ion homeostasis; IMP.
DR GO: GO:0007047; P:cell ion homeostasis; IMP.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR001125; Recoverin.
DR Pfam: PF00036; ehand; 4.
DR PRINTS: PR00450; RECOVERIN.
DR PRODOM: PD000012; EF-hand; 2.
DR SMART: SM00054; EFN; 4.
DR PROSITE: PS00018; EF_HAND; 4.
KW Calcium-binding; Repeat; Myristate;
FT INTL MET 0
FT LIPID 1 MYRISTATE.
FT CA_BIND 33 44 EF-HAND 1 (BY SIMILARITY).
FT CA_BIND 65 76 EF-HAND 2 (BY SIMILARITY).
FT CA_BIND 102 113 EF-HAND 3 (BY SIMILARITY).
FT CA_BIND 143 154 EF-HAND 4 (BY SIMILARITY).
SQ SEQUENCE 174 AA; 19508 MW; ECF0109744FCERO CRC64;

Query Match 19.8%; Score 179.5; DB-1; Length 174;
Best Local Similarity 23.3%; Pred. No. 2.2e-06;
Matches 41; Conservative 55; Mismatches 63; Indels 17; Gaps 4;

QY 2 GSGSRKSEKELAEYODTLFTRKQELLAHRRFCELLPQEGRTVESSIRAAVPEQLIST 61
DB 1 GAAPSKIVDGLLED---TFNDREITERLKRKFLKLDSSGSDKN-----EFVSI 48
QY 62 PELKANPFRKICRVFSTSPAKDSLSFEFDLLSVFSDTATPDIKSHYAFRIFDDDD 121
DB 49 IPVSASNPPLASRLFSVYDEGGD-VDFQEFITGTSFSGRSKDEKLRFAFKYIDDD 107
QY 122 TNLNREDLSRLVNCITGEGEDTRLASASEMKOLIDNILEXXXXXXXQXQHVIR 177
DB 108 FISNGELIYLVKMWG-----SNLDEDOLOQIVDKRTIVENDSDGGRISFEFFKNAI 159

RESULT 9
CALB_NEUCR STANDARD; PRT; 174 AA.
ID CALB_NEUCR STANDARD; PRT; 174 AA.
AC P87072; O13408;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calcineurin B subunit (Protein phosphatase 2B regulatory subunit)
GN CNB-1 OR CAN-B.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=74A;
RX MEDLINE=98007857; PubMed=9349701;

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RA Prokisch H., Yarden O., Dieminger M., Trotschug M., Barthelmeß I.B.;
 RT "Impairment of calcineurin function in Neurospora crassa reveals its
 RT essential role in hyphal growth, morphology and maintenance of the
 RT apical Ca²⁺ gradient.";
 RL Mol. Gen. Genet. 256:104-114(1997).
 RN (2)
 RN SEQUENCE FROM N.A.
 RX MEDLINE=98345933; PubMed=9680955;
 RA Kothe G.O., Free S.J.;
 RT "Calcineurin subunit B is required for normal vegetative growth in
 RT Neurospora crassa.";
 RL Fungal Genet. Biol. 23:248-258(1998).
 CC -1- FUNCTION: REGULATOR SUBUNIT OF CALCINEURIN, A CALCIUM-DEPENDENT,
 CC CALMODULIN STIMULATED PROTEIN PHOSPHATASE. CONFERS CALCIUM
 CC SENSITIVITY.
 CC -1- SUBUNIT: COMPOSED OF A CATALYTIC SUBUNIT (A) AND A REGULATORY
 CC SUBUNIT (B).
 CC -1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
 CC SITES.
 CC -1- SIMILARITY: Contains 4 EF-hand calcium-binding domains.
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 CC -----
 DR EMBL: Y12814; CAA73345.1;
 DR EMBL: AF034089; AAB87526.1;
 DR PIR: T47245; T47245.
 DR HSP: P06705; IAU1.
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR001125; Recoverin.
 DR Pfam: PF00036; ehand; 4.
 DR PRINTS: PR00450; RECOVERIN.
 DR PRODOM: PD000012; EF-hand; 2.
 DR SMART: SM00054; EFh; 4.
 DR PROSITE: PS00018; EF_HAND; 4.
 DR K: K01111; EF-hand.
 KW Calcium-binding; Repeat.
 FT CA_BIND 34 45 EF-HAND 1 (BY SIMILARITY).
 FT CA_BIND 66 77 EF-HAND 2 (BY SIMILARITY).
 FT CA_BIND 103 114 EF-HAND 3 (BY SIMILARITY).
 FT CA_BIND 144 155 EF-HAND 4 (BY SIMILARITY).
 FT CONFLICT 9 9 P -> L (IN REF. 2).
 FT CONFLICT 28 28 K -> M (IN REF. 2).
 FT CONFLICT 68 68 N -> D (IN REF. 2).
 FT CONFLICT 87 87 R -> S (IN REF. 2).
 FT CONFLICT 134 134 R -> Q (IN REF. 2).
 FT CONFLICT 164 174 DVSMSMTLDOF -> ECHO (IN REF. 2).
 SQ SEQUENCE 174 AA; 19849 MW; F5093B7869B7B710 CRC64;
 Query Match 18.7%; Score 169.5; DB 1; Length 174;
 Best Local Similarity 21.7%; Pred. No. 1.3e-05;
 Matches 34; Conservative 52; Mismatches 58; Indels 13; Gaps 3;
 QY 24 KQELIAHRRFCELLPQEQRTVESSLRAQVPEQILSLPELKNPFRKICRVFSSPAK 83
 DB 20 REEVDRLRRFRMKLDKNSGTIER-----EFISLQIISNPATRIATIAFDENGG 71
 QY 84 DLSLFEFDLDSVSDTATPDIKSHYARIFEDDDGTLNREDLSRLVNCUUGEEDPR 143
 DB 72 D-VDFEFGSLASFSRKNKQKLFARFYDIDRDGYISNGELFVLKMYG-----SN 126
 QY 144 LSASEKQIDNILEXXXXXXXXXXXXXQYVHS 180
 DB 127 LKQQLQRIVDKTIHEADLDKDKGISFEFTKMENT 163
 RESULT 10
 CALB_HUMAN STANDARD: PRT; 169 AA.

AC P06705; P15117; Q08044;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Calcineurin B subunit isoform 1 (Protein phosphatase 2B regulatory
 DE subunit 1) (Protein phosphatase 3 regulatory subunit B alpha isoform
 DE 1).
 GN PPP3R1 OR CNB OR CNA2.
 OS Homo sapiens (Human).
 OS Bos taurus (Bovine), and
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606, 9913, 10116;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC SPECIES-Human;
 RX MEDLINE=90126237; PubMed=255868;
 RA Guerini D., Krinks M.H., Sikela J.M., Hahn W.E., Klee C.B.;
 RT "Isolation and sequence of a cDNA clone for human calcineurin B, the
 RT Ca²⁺-binding subunit of the Ca²⁺/calmodulin-stimulated protein
 RT phosphatase.";
 RL DNA 8:675-682(1989).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC SPECIES-Bovine;
 RA Nargang C.E., Bottorff D.A., Adachi K.;
 RL Submitted (APR-1993) to the EMBL/GenBank/DBJ databases.
 RN (3)
 RP SEQUENCE OF 1-168.
 RC SPECIES-Bovine; TISSUE-Brain;
 RX MEDLINE=84132092; PubMed=6321184;
 RA Altken A., Klee C.B., Cohen P.;
 RT "The structure of the B subunit of calcineurin.";
 RL Eur. J. Biochem. 139:663-671(1984).
 RN (4)
 RP SEQUENCE FROM N.A.
 RC SPECIES-Rat;
 RA Perrino B.A., Huang X., Ng L.Y., Soderling T.R.;
 RL Submitted (XXX-1992) to the EMBL/GenBank/DBJ databases.
 RN (5)
 RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.
 RC SPECIES-Rat; TISSUE-Brain, and Testis;
 RX MEDLINE=94153993; PubMed=8110831;
 RA Chang C.-D., Mukai H., Kuno T., Tanaka C.;
 RT "cDNA cloning of an alternatively spliced isoform of the regulatory
 RT subunit of Ca²⁺/calmodulin-dependent protein phosphatase (calcineurin
 RT B alpha 2).";
 RL Biochim. Biophys. Acta 1217:174-180(1994).
 RN (6)
 RP CALCIUM-BINDING DATA.
 RC SPECIES-Bovine;
 RX MEDLINE=80101597; PubMed=293720;
 RA Klee C.B., Crouch T.H., Krinks M.H.;
 RT "Calcineurin: a calcium- and calmodulin-binding protein of the
 RT nervous system.";
 RL Proc. Natl. Acad. Sci. U.S.A. 76:6270-6273(1979).
 RN (7)
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RC SPECIES-Bovine;
 RX MEDLINE=95360994; PubMed=7543369;
 RA Griffith J.P., Kim J.L., Kim E.E., Sincchak M.D., Thomson J.A.,
 RT Fitzgibbon M.J., Fleming M.A., Caron P.R., Hsiao K., Navia M.A.;
 RT "X-ray structure of calcineurin inhibited by the immunophilin-
 RT immunosuppressant FKBP12-FK506 complex.";
 RL Cell 82:507-522(1995).
 RN (8)
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
 RC SPECIES-Human;
 RX MEDLINE=96097077; PubMed=8524402;
 RA Kissinger C.R., Parge H.E., Knighton D.R., Lewis C.T., Pelletier L.A.,
 RA Tempczyk A., Kallish V.J., Tucker K.D., Showalter R.E., Moomaw E.W.,
 RA Gastinel L.N., Habuka N., Chen X., Maldonado F., Barker J.E.,

RA Baquet R., Villafranca J.E.;
 RT "Crystal structures of human calcineurin and the human FKBP12-FK506-
 CC calcineurin complex";
 RL Nature 378:641-644(1995).
 CC -1- FUNCTION: REGULATORY SUBUNIT OF CALCINEURIN, A CALCIUM-DEPENDENT,
 CC CALMODULIN STIMULATED PROTEIN PHOSPHATASE. CONFERS CALCIUM
 CC SENSITIVITY.
 CC -1- SUBUNIT: COMPOSED OF A CATALYTIC SUBUNIT (A) AND A REGULATORY
 CC SUBUNIT (B).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named Isoforms-2;
 CC Name-1;
 CC IsoId-P06705-1; Sequence-Displayed;
 CC Name-2;
 CC IsoId-P06705-2; Sequence-VSP-000729;
 CC Note-Has been shown to exist only in rat so far;
 CC -1- TISSUE SPECIFICITY: ISOFORM 2 IS TESTIS-SPECIFIC.
 CC -1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
 CC SITES.
 CC -1- SIMILARITY: Contains 4 EF-hand calcium-binding domains.
 CC -----
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 CC -----
 DR EMBL: M30773; AAB08721.1; -;
 DR EMBL: X71666; CAA50659.1; -;
 DR EMBL: L03554; AAA04854.1; -;
 DR EMBL: D14568; BAA03422.1; -;
 DR EMBL: D14425; BAA03318.1; -;
 DR PIR: A33391; A33391.
 DR PIR: I45831; S34127.
 DR PIR: S42716; S42716.
 DR PDB: LAUI; 03-DEC-97.
 DR PDB: LTCO; 12-FEB-97.
 DR PDB: IM63; 25-SEP-02.
 DR PDB: IMF8; 23-OCT-02.
 DR Genew; HGNC:9317; PPP3R1.
 DR MIM: 601302; -;
 DR GO: GO:0005955; C:calcineurin complex; NAS.
 DR GO: GO:0005509; F:calcium ion binding activity; NAS.
 DR GO: GO:0004723; F:calcium-dependent protein serine/threonine kinase activity; NAS.
 DR GO: GO:0005517; F:calmodulin inhibitor activity; NAS.
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR001125; Recoverin.
 DR Pfam: PF00036; ehand; 4.
 DR PRINTS: PR00450; RECOVERIN.
 DR PRODOM: PD000012; EF-hand; 2.
 DR SMART: SM00054; Efh; 4.
 DR PROSITE: PS00018; EF-HAND; 4.
 KM Calcium-binding; Repeat; Alternative splicing; Myristate;
 KW 3D-structure.
 FT INT_MET 0 0
 FT LIPID 1 1 MYRISTATE.
 FT CA_BIND 30 41 EF-HAND 1.
 FT CA_BIND 62 73 EF-HAND 2.
 FT CA_BIND 99 110 EF-HAND 3.
 FT CA_BIND 140 151 EF-HAND 4.
 FT VARSPIC 1 1
 G -> MEQGTDLDSQIFPPPEKFNWKKGRHFRONKYPFSR
 ELYNLPADNRKG (in isoform 2).
 /FTID-VSP-000729.
 C -> M (in REF. 3).
 C -> S (in REF. 3).
 FT CONFLICT 11 11
 FT CONFLICT 153 153
 FT HELIX 16 29
 FT TURN 31 32
 FT STRAND 36 37
 FT HELIX 39 42
 FT TURN 43 44
 FT HELIX 46 49

FT TURN 50 50
 FT TURN 52 53
 FT HELIX 54 61
 FT TURN 63 64
 FT STRAND 69 70
 FT HELIX 71 78
 FT HELIX 79 81
 FT TURN 83 84
 FT HELIX 87 98
 FT TURN 100 101
 FT STRAND 105 106
 FT HELIX 108 119
 FT TURN 120 121
 FT HELIX 125 139
 FT TURN 141 142
 FT STRAND 147 148
 FT HELIX 149 156
 FT HELIX 157 159
 FT HELIX 161 164
 SQ SEQUENCE 169 AA; 19169 MW; 749141BD0434C90C CRC64;
 Query Match 18.3%; Score 165.5; DB 1; Length 169;
 Best Local Similarity 25.4%; Pred. No. 2.4e-05;
 Matches 31; Conservative 44; Mismatches 42; Indels 5; Gaps 2;
 QY 56 EQLSLDELKANKPKERICRFRSTSPAKDSLSFEDFDLDSVFSDTAPDKSHYAFRI 115
 DQ 40 EEFMSLELQNPVQVRVIDFDPD-GNGEYDFKEFTLEGVSQFSVKGDKGEOLKPAFRIV 98
 QY 116 DFDDDDGTINREDLSRLVNCUTGEGEDTRLASERKQDINILEEXXXXXXXXHXOH 175
 DQ 99 DMDKGYISNGELPQVAKMWG-----NNLKRTQIQQIVDKTIINADKDGGRISFEERCA 154
 QY 176 VI 177
 DQ 155 VV 156
 RESULT 11
 CALB_MOUSE
 ID CALB_MOUSE STANDARD: PRT; 169 AA.
 AC 063810;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Calcineurin B subunit isoform 1 (Protein phosphatase 2B regulatory
 DE subunit 1) (Protein phosphatase 3 regulatory subunit B alpha isoform
 DE 1).
 GN PPP3R1 OR CNB.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=92392379; PubMed=1325794;
 RA Ueki K., Muramatsu T., Kincaid R.L.;
 RT "Structure and expression of two isoforms of the murine calmodulin-
 RT dependent protein phosphatase regulatory subunit (calcineurin B).";
 RL Biochem. Biophys. Res. Commun. 187:537-543(1992).
 CC -1- FUNCTION: REGULATORY SUBUNIT OF CALCINEURIN, A CALCIUM-DEPENDENT,
 CC CALMODULIN STIMULATED PROTEIN PHOSPHATASE. CONFERS CALCIUM
 CC SENSITIVITY.
 CC -1- SUBUNIT: COMPOSED OF A CATALYTIC SUBUNIT (A) AND A REGULATORY
 CC SUBUNIT (B).
 CC -1- TISSUE SPECIFICITY: Brain-specific.
 CC -1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
 CC SITES.
 CC -1- SIMILARITY: Contains 4 EF-hand calcium-binding domains.
 CC -----
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CC EMBL: S43864; AAB23171.1; -
 DR PIR: JCI220; JCI220.
 DR HSSP: P06705; IAU1.
 DR MGD: MGI:107172; Ppp3r1.
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR001125; Recoverin.
 DR Pfam: PF00036; ehand; 4.
 DR PRINTS: PR00450; RECOVERIN.
 DR PRODOM: PD000012; EF-hand; 2.
 DR SMART: SM00054; EFh; 4.
 DR PROSITE: PS00018; EF-HAND; 4.
 DR Calcium-binding; Repeat; Myristate.
 KW INT_MET 0
 FT LIPID 1
 FT CA_BIND 30 41 EF-HAND 1.
 FT CA_BIND 62 73 EF-HAND 2.
 FT CA_BIND 99 110 EF-HAND 3.
 FT CA_BIND 140 151 EF-HAND 4.
 SO SEQUENCE 169 AA; 19142 MW; D1490BASHD2P432F CRC64;

Query Match 18.3%; Score 165.5; DB 1; Length 169;
 Best Local Similarity 25.4%; Pred. No. 2.4e-05;
 Matches 31; Conservative 44; Mismatches 42; Indels 5; Gaps 2;

QY 56 EQILSPFLANPKPKRICKRFTSTSPAKDLSLFEFDLILSVFSDTAPDICKSHYARIF 115
 Db 40 EEFWSLPDLQONPLVGVIVIDIFPD -GNGEVDKEFELEGVSQFVKDKDEKLFARIT 98
 QY 116 DFDDGDLNEDLSRLVNCILGSEEDRLSASENKQILDLILEEXXXXXXXXHXH 175
 Db 99 DMDGYSNGELFQVLYKAVG---NNLKDTQLQIVDKTIINADKDGDRISFEFCA 154
 QY 176 VI 177
 Db 155 VV 156

RESULT 12
 CA22_MOUSE STANDARD; PRT; 194 AA.
 AC 062877;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Calcium-binding protein p22 (Calcium-binding protein CHP) (Calcineurin homologous protein) (sld470).
 GN CHP.
 OS Mus musculus (Mouse), and
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090, 10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES-Rat: TISSUE-Liver;
 RX MEDLINE=96215311; PubMed=8626580;
 RA Barroso M.R., Bernd K.K., Dewitt N.D., Chang A., Mills K.,
 RA Stul E.S.;
 RT "A novel Ca²⁺-binding protein, p22, is required for constitutive membrane traffic."
 RL J. Biol. Chem. 271:10183-10187(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES-Rat: TISSUE-Brain;
 RX MEDLINE=21374135; PubMed=11481038;
 RA Matsumoto M., Miyake Y., Nagita M., Inoue H., Shitakubo D.,
 RA Takemoto K., Ohtsuka C., Murakami H., Nakamura N., Kanazawa H.;

"A serine/threonine kinase which causes apoptosis-like cell death interacts with a calcineurin B-like protein capable of binding Na⁺/H⁺ exchanger".
 J. Biochem. 130:217-225(2001).
 [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES-Mouse;
 RA Seki N., Hattori A., Hayashi A., Kozuma S., Muramatsu M., Saito T.;
 RL Submitted (MAR-1999) to the EMBL/Genbank/DBJ databases.
 [4]
 RP SEQUENCE FROM N.A.
 RC SPECIES-Mouse; STRAIN=C57BL/6J; TISSUE=Liver;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mommaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilmink L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohlsuki S.,
 RA Hqashshazaki Y.;
 RL "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 CC -1- FUNCTION: REQUIRED FOR CONSTITUTIVE MEMBRANE TRAFFIC.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: Ubiquitously expressed.
 CC -1- PM: BOTH N-MYRISTOYLATION AND CALCIUM-MEDIATED CONFORMATIONAL CHANGES ARE ESSENTIAL FOR ITS FUNCTION.
 CC -1- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
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CC EMBL: U39875; AAB04146.1; -
 DR EMBL: AB070350; BAB63369.1; -
 DR EMBL: AB025217; BAA84688.1; -
 DR EMBL: AK005067; BAB23791.1; -
 DR HSSP: P06705; IAU1.
 DR MGD: MGI:1927185; Chp.
 DR InterPro: IPR002048; EF-hand.
 DR Pfam: PF00036; ehand; 3.
 DR PRODOM: PD000012; EF-hand; 2.
 DR SMART: SM00054; EFh; 2.
 DR PROSITE: PS00018; EF-HAND; 1.
 KW Calcium-binding; Repeat; Myristate.
 FT INIT_MET 0
 FT LIPID 1
 FT DOMAIN 38 49 MYRISTATE (PROBABLE).
 FT DOMAIN 70 81 ANCESTRAL CALCIUM SITE 1 (POTENTIAL).
 FT CA_BIND 122 133 EF-HAND 3 (BY SIMILARITY).
 FT CA_BIND 163 174 EF-HAND 4 (BY SIMILARITY).
 FT MYRAGEN 133 133 E->A: LOSS OF TARGETING/FUSION FUNCTION.
 SO SEQUENCE 194 AA; 22301 MW; E2DF3E5F627B8231 CRC64;

Query Match 17.8%; Score 161; DB 1; Length 194;
 Best Local Similarity 23.7%; Pred. No. 6.4e-05;
 Matches 46; Conservative 46; Mismatches 70; Indels 32; Gaps 6;

DR EMBL: L33681; AAA85632.1; -
 DR EMBL: 280216; CAB02282.1; -
 DR PIR: T20725; T20725.
 DR HSSP: P36610; IGB1.
 DR Wormep; F10G8.5; CE09340.
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR001125; Recoverin.
 DR Pfam: PF00036; ehand.3.
 DR PRINTS: PR00450; RECOVERIN.
 DR ProDom: PD000012; EF-hand; 1.
 DR SMART: SM00054; EFh; 3.
 DR PROSITE: PS00018; EF_HAND; 3.
 DR K1 Calcium-binding.
 DR INT MET 0 BY SIMILARITY.
 FT DOMAIN 37 48 ANCESTRAL CALCIUM SITE 1.
 FT CA_BIND 74 85 EF-HAND 2 (POTENTIAL).
 FT CA_BIND 110 121 EF-HAND 3 (POTENTIAL).
 FT CA_BIND 157 168 EF-HAND 4 (POTENTIAL).
 SQ SEQUENCE 189 AA; 21854 MW; 5EP87155289F735 CRC64;

Query Match 17.2%; Score 156; DB 1; Length 189;
 Best Local Similarity 22.6%; Pred. No. 0.00015;
 Matches 44; Conservative 50; Mismatches 67; Indels 34; Gaps 5;

OY 3 GSGSRSLKELLAEYQDITFLTKQKILLAHRRFCCLLPQEQRTVSSLRAGVPEFOILSLP 62
 DB 4 GSKRLSKEDLEFLKKTNTFEQIKWKYGFVQDCPKGLHTKQGIKIVYDF-----FP 58
 OY 63 ELKANPKEKICRYFSTSPAKDSLSFEDLDLSVFSSTA--PDISHVAFRIFDDDD 120
 DB 59 SGSGAEKCEHVFRTFD-----DMSGFIDFEFLAIIVNTSSGTEPKLEMAFRMYDIDGN 114
 OY 121 GTLNREDLSRLVNL-----TGEGEDTRLSASEM-----KOLIDNIL 157
 DB 115 GTIDKEKMIKIIIEAIYEMLGPEYTKSADSPKRAKAMIFEMKDVNNDEKLTKEFVDCGL 174
 OY 158 EEXXXXXXXXKXKX 172
 DB 175 ADKELFOILTNEVK 189

RESULT 15
 CA22 HUMAN STANDARD; PRT; 194 AA.
 AC Q99635;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Calcium-binding protein p22 (Calcium-binding protein CHP) (Calcineurin homologous protein) (Calcineurin B homolog).
 GN CHP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-cell;
 RX MEDLINE=97057295; PubMed=8901634;
 RA Lin X., Barber D.L.;
 RT "A calcineurin homologous protein inhibits GTPase-stimulated Na-H exchange."
 RL Proc. Natl. Acad. Sci. U.S.A. 93:12631-12636(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Muscle;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strusberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemen G.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Dlatanchko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulix S.W., Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Helton E., Kellerman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E., Jones S.J.M., Maira M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences".
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL
 CC - FUNCTION: REQUIRED FOR CONSTITUTIVE MEMBRANE TRAFFIC (BY SIMILARITY). INHIBITS GTPASE-STIMULATED NA-H EXCHANGE SPECIFICALLY BINDS TO THE SODIUM/HYDROGEN EXCHANGER 1 (NHE1) AT A DOMAIN THAT IS CRITICAL FOR GROWTH FACTOR STIMULATION OF EXCHANGE ACTIVITY.
 CC - SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC - TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED. HAS BEEN FOUND IN FETAL EYE, LONG, LIVER, MUSCLE, HEART, KIDNEY, THYMUS AND SPLEEN.
 CC - PTM: BOTH N-MYRISTOYLATION AND CALCIUM-MEDIATED CONFORMATIONAL CHANGES ARE ESSENTIAL FOR ITS FUNCTION IN EXOCYTIC TRAFFIC (BY SIMILARITY).
 CC - PTM: PHOSPHORYLATED IN VIVO. DECREASE IN ITS PHOSPHORYLATION IS ASSOCIATED WITH AN INCREASE IN EXCHANGE ACTIVITY. THE PHOSPHORYLATION STATE MAY REGULATE THE BINDING TO NHE1.
 CC - SIMILARITY: Contains 2 EF-hand calcium-binding domains.
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DR EMBL: U61538; AAB37770.1; -
 DR EMBL: BC001646; AAH01646.1; -
 DR HSSP: P06705; IAU1.
 DR MIM: 606988; -
 DR GO: GO:0015459; F:potassium channel regulator activity; TAS.
 DR GO: GO:0006813; P:potassium ion transport; TAS.
 DR GO: GO:0007264; P:small GTPase mediated signal transduction; TAS.
 DR InterPro: IPR002048; EF-hand.
 DR Pfam: PF00036; ehand; 3
 DR ProDom: PD000012; EF-hand; 2.
 DR SMART: SM00054; EFh; 2.
 DR PROSITE: PS00018; EF_HAND; FALSE-NEG.
 KW Calcium-binding; Repeat; Myristate; Phosphorylation.
 FT INIT MET 0 BY SIMILARITY.
 FT LIPID 1 MYRISTATE (BY SIMILARITY).
 FT DOMAIN 38 49 ANCESTRAL CALCIUM SITE 1 (POTENTIAL).
 FT DOMAIN 70 81 ANCESTRAL CALCIUM SITE 2 (POTENTIAL).
 FT CA_BIND 122 133 EF-HAND 3 (BY SIMILARITY).
 FT CA_BIND 163 174 EF-HAND 4 (BY SIMILARITY).
 SQ SEQUENCE 194 AA; 22325 MW; 17DDE5F03088380 CRC64;

Query Match 17.2%; Score 156; DB 1; Length 194;
 Best Local Similarity 23.2%; Pred. No. 0.00015;
 Matches 45; Conservative 46; Mismatches 71; Indels 32; Gaps 6;

OY 5 GSR-----LSKELLAEYQDITFLTKQKILLAHRRFCCLLPQEQRTVSSLRAGVPEFOILSLP 60
 DB 1 GSRASLLDDELEEFKKTGFSHSQITRLYSRFTSLDGENCTLSR-----EDFOR 52
 OY 61 LPELANPKEKICRYFSTSPAKDSLSFEDLDLSVFSSTA--PDISHVAFRIFDDDD 105
 DB 53 IPELANPGLGRITINAFPE-GEQVNFEGFMKTLAHFRPIEDENSKVNGDEPELNSNS 111
 OY 106 IKSHVAFRIFDDDDGDTLNREDLSRLVNLCTGEGEDTRLSASEMKNOLIDNILEXXXXXX 165

Db 112 NKLHFAFRLYDLKDDEKISRDELQVLRMWG---VNISDEQLGIADRTIQEADQDGD 167

Oy 166 XXXXXXXXQHYISR 179
::: 1: :

Db 168 SAISFEFEVKYLEK 181

Search completed: July 24, 2003, 13:18:34
Job time : 25 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 24, 2003, 12:55:51 ; Search time 95 Seconds

(without alignments)
518.822 Million cell updates/sec

Title: SEQ2_MOD

Perfect score: 905

Sequence: 1 MGSGSRLSKELLAEYODLT.....XXQHVISRSPDFASSRKIVL 191

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL_23:*
1: sp-archaea:*
2: sp-bacteria:*
3: sp-fungi:*
4: sp-human:*
5: sp-invertebrate:*
6: sp-mammal:*
7: sp-mhc:*
8: sp-organelle:*
9: sp-phage:*
10: sp-plant:*
11: sp-rodent:*
12: sp-virus:*
13: sp-vertebrate:*
14: sp-unclassified:*
15: sp-rylous:*
16: sp-bacteriap:*
17: sp-archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	611	67.5	143	11 Q8C2K4	Q8C2K4 mus musculi
2	385	42.5	311	5 Q93640	Q93640 caenorhabdi
3	342	37.8	185	11 Q9D9N5	Q9D9N5 mus musculu
4	325	35.9	187	4 Q96077	Q96077 homo sapien
5	318.5	35.2	206	5 Q9W205	Q9W205 drosophila
6	277	30.6	54	6 Q9GLJ2	Q9GLJ2 sus scrofa
7	201.5	22.3	180	5 Q9GP83	Q9GP83 dictyosteli
8	193	21.3	175	10 Q93VF2	Q93VF2 eucalyptus
9	190	21.0	175	10 Q9LS47	Q9LS47 arabidopsis
10	188	20.8	175	10 Q9L8K7	Q9L8K7 arabidopsis
11	175.5	19.4	189	5 Q9VNF9	Q9VNF9 drosophila
12	174	19.2	175	5 Q9U0X7	Q9U0X7 leishmania
13	170	18.8	177	5 Q8M0T6	Q8M0T6 toxoplasma
14	170	18.8	200	5 Q8SFR6	Q8SFR6 encephalito
15	167.5	18.5	171	5 Q20804	Q20804 caenorhabdi
16	166.5	18.4	187	5 Q9VWX8	Q9VWX8 drosophila

17	163.5	18.1	169	5 Q9NFN1	Q9NFN1 schistosoma
18	158.5	17.5	191	11 Q8C6H3	Q8C6H3 mus musculu
19	157.5	17.4	170	5 Q9NKW7	Q9NKW7 patinopecte
20	157.5	17.4	170	5 Q9SP81	Q9SP81 bombyx mori
21	156.5	17.3	115	11 Q99LO9	Q99LO9 mus musculu
22	156	17.2	214	11 Q8VCN1	Q8VCN1 mus musculu
23	154	17.0	175	3 Q9HDE1	Q9HDE1 cryptococcu
24	154	17.0	177	3 Q9HDD3	Q9HDD3 cryptococcu
25	153.5	17.0	226	10 Q81446	Q81446 arabidopsis
26	152.5	16.9	226	10 Q8LAS7	Q8LAS7 arabidopsis
27	152	16.8	170	4 Q8WYJ4	Q8WYJ4 homo sapien
28	152	16.8	173	4 Q961Z3	Q961Z3 homo sapien
29	150.5	16.6	161	10 Q9AY39	Q9AY39 oryza sativ
30	150	16.6	190	5 Q9NAY9	Q9NAY9 naegleria f
31	148	16.4	179	5 Q8IRV9	Q8IRV9 plasmodium
32	147	16.2	225	10 Q8L7F6	Q8L7F6 plasmodium
33	145.5	16.1	213	5 Q16343	Q16343 caenorhabdi
34	143.5	15.9	190	3 Q8TGC0	Q8TGC0 magnaporthe
35	143.5	15.9	190	3 Q96X50	Q96X50 magnaporthe
36	143	15.8	225	10 Q8W5C8	Q8W5C8 oryza sativ
37	143	15.8	274	10 Q9AMM4	Q9AMM4 oryza sativ
38	142.5	15.7	213	10 Q9L7B8	Q9L7B8 arabidopsis
39	141.5	15.6	226	10 Q81447	Q81447 arabidopsis
40	140.5	15.5	195	5 Q23643	Q23643 caenorhabdi
41	140.5	15.5	231	11 Q9DAJ7	Q9DAJ7 mus musculu
42	140	15.5	29	11 Q99JY5	Q99JY5 mus musculu
43	137	15.1	1551	6 Q9MZF4	Q9MZF4 canis famli
44	136.5	15.1	1553	6 Q8HZK3	Q8HZK3 sus scrofa
45	135.5	15.0	213	10 Q81445	Q81445 arabidopsis

ALIGNMENTS

RESULT 1

ID Q8C2K4 PRELIMINARY; PRT; 143 AA.
AC Q8C2K4;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Calcium and integrin binding.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MOD; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team.
RT "Analysis of the mouse transcriptome based on functional annotation of
RL Nature 420:563-573(2002).
DR EMBL; AK088450; BAC40359.1;
SQ SEQUENCE 143 AA; 16076 MW; E01618686F496057 CRC64;

Query Match 67.5%; Score 611; DB 11; Length 143;
Best Local Similarity 64.9%; Pred. No. 3.8e-42;
Matches 124; Conservative 17; Mismatches 2; Indels 48; Gaps 1;

QY	1	MGSGSRLSKELLAEYODLTFLTKQELLAHRRFCPELLPOEDRTVESSIRAAVPEFQILS	60
DB	1	MGSGSRLSKELLAEYODLTFLTKQELLAHRRFCPELLPOEDRTVESSIRAAVPEFQILS	60
QY	61	LPELKANPKERICKVFSTSPAKDSLSEDFDLTVSVDATPDPIKSHYARIFDFDD	120
DB	18	-----ANFKERIKVWFSTSPRDSLFEDFDLTVSVDATPDPIKSHYARIFDFDD	72
QY	121	GTINREDLSRLVNCITGEGEDTRLASSEMQLINDILEBXXXXXXXQXIVISRS	180
DB	73	GTLDREDSQLVNCITGEGEDTRLASSEMQLINDILEBXXXXXXXQXIVISRS	132

QY 181 PDFASSFRVL 191
 DB 133 PDFASSFRVL 143

RESULT 2

Q93640 PRELIMINARY: PRT: 311 AA.
 AC Q93640:
 DT 01-FEB-1997 (TREMblrel. 02, Created)
 DT 01-FEB-1997 (TREMblrel. 02, Last sequence update)
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
 DE F30A10.1 protein.
 GN F30A10.1
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 NX NCBI_TaxID=6239;
 RA [1]
 RP SEQUENCE FROM N.A.
 RA Barlow K.;
 RL Submitted (OCT-1996) to the EMBL/Genbank/DBJ databases.
 RP [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C. elegans: A platform for
 RT investigating biology".
 RL Science 282:2012-2018(1998).
 DR EMBL; 281072; CAB03019.1; -
 DR HSSP; Q99828; IDGV.
 DR WormPep; F30A10.1; CE09802.
 DR InterPro; IPR002048; EF-hand.
 DR Pfam; PF00036; efhand; 3.
 DR ProDom; PD000012; EF-hand; 1.
 DR SMART; SM00054; EFh; 2.
 SO SEQUENCE 311 AA; 35960 MW; 97AFA56A6F526F CRC64;

Query Match 42.5%; Score 385; DB 5; Length 311;
 Best Local Similarity 39.1%; Pred. No. 4.5e-23;
 Matches 81; Conservative 51; Mismatches 49; Indels 26; Gaps 5;

QY 1 MGSGSRLS-----KELLAEYODLFLTKOELLARHRCFELLPQOQRTYSS 48
 DB 111 MGNASSISELNLFSKGVFTREQLDEQDCTFTTRDIILKYRFALNKHK---VPTN 167
 QY 49 LRAQV-----EQIILSLPELKNPFRERICRVFSTSPAKDSLSFEDFLDLVSFSDTA 102
 DB 168 MGNRPATITLTFEEVERKMPLEKPNPKRRICEVFS-EDGRGNLSFDFLDMFVSFSEMA 226
 QY 103 TPDIKSHVAFRIFFDDGDTLNREDLSRLVNCITGEGEDFRLSASEMKOLINDLLEEXX 162
 DB 227 PLOKAKTARIRIYIDDELGHDLDSKMSLSTRD---ELSDVEVEFITERITEADL 282
 QY 163 XXXXXXXXXXXXQHVISRPDPASSFKI 189
 DB 283 DGDSSINFAEEFHVSRSPDFIRTEHI 309

RESULT 3

Q9D9N5 PRELIMINARY: PRT: 185 AA.
 AC Q9D9N5:
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
 DE 1700041E20RIK protein.
 GN 1700041E20RIK
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NX NCBI_TaxID=10090;

RP [1]
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamada I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Felschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schiml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Balarelli R., Barish G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyokawa K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
 RA Wyszewski A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 DR EMBL; AK006670; BAB24697.1; -
 DR HSSP; Q99828; IDGV.
 DR MGP; MGI:1920509; 1700041E20RIK.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR001125; Recoverin.
 DR Pfam; PF00036; efhand; 2.
 DR PRINTS; PR00450; RECOVERIN.
 DR ProDom; PD000012; EF-hand; 1.
 DR SMART; SM00054; EFh; 2.
 DR ProSite; PS00018; EF-HAND; 1.
 SO SEQUENCE 185 AA; 21637 MW; 70C6B3BEF73844CB CRC64;

Query Match 37.8%; Score 342; DB 11; Length 185;
 Best Local Similarity 40.3%; Pred. No. 6.9e-20;
 Matches 73; Conservative 48; Mismatches 46; Indels 14; Gaps 5;

QY 11 ELAEOYDPLFLTKOELLARHRCFELLPQOQRTYSSLRQAVPEQIILSLPELKNPFK 70
 DB 12 EDLEEQALFTLRNELLCHIDFLKLCPSKHYKEAL---TMDVSSLPALAVNPF 67
 QY 71 ERICRVSTSPAKDSLSFEDFLDLVSFSDTAPEIKSHVAFRIFFDDGTLNREDLSR 130
 DB 68 DRICRVSHD---NVFSFEDVIGMAVSFSEQACPSLKEIVAFRIYDFNENGFIDEDLEE 124
 QY 131 LVNCITGEGEDFRLSASE--KCOLINDLLEEXXXXXXXXQHVISRPDPASSFK 188
 DB 125 IVLRL-KSD----ASEDLMDVHHLVLSQDLDNDMSLSPSEFHAMASPDPMNSFR 179
 QY 189 I 189
 DB 180 I 180

RESULT 4

Q96Q77 PRELIMINARY: PRT: 187 AA.
 AC Q96Q77:
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
 DE KIP3.
 GN KIP3
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NX NCBI_TaxID=9606;
 RA [1]
 RP SEQUENCE FROM N.A.
 RA Hayashi A., Okaze H., Kozuma S., Saito T.;

RT "Full Length cDNA of gene At3g18430 (GI:15229640).";
 RN Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE FROM N.A.
 RA Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
 RA Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
 RA Tang C., Totilunt M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
 RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
 RA Kamita A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
 RA Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
 RA Sakurai T., Saeon M., Seki M., Shinn P., Southwick A., Shinozaki K.,
 RA Davis R.M., Ecker J.R., Theologis A.,
 RT Arabidopsis Open Reading Frame (ORF) Clones."
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB026658; BAB01109.1;
 DR EMBL: AY061378; AAL36096.1;
 DR EMBL: AY091287; AAM14226.1;
 DR HSP: P06705; IAO1.
 DR InterPro: IPR002048; EF-hand.
 DR Pfam: PF00036; efhand; 2.
 DR ProDom: PD000012; EF-hand; 1.
 DR PROSITE: PS00018; EF_HAND; 1.
 KW Hypothetical protein
 SQ SEQUENCE 175 AA; 20032 MW; B26D7E2ADA37AFED CRC64;
 Query Match 21.0%; Score 190; DB 10; Length 175;
 Best Local Similarity 25.0%; Pred. No. 1.9e-07;
 Matches 46; Conservative 57; Mismatches 57; Indels 24; Gaps 5;
 QY 1 MGSGSRSLKELIAEYQ---DLTFLTKQELLAHRRFCELLPQEQRTVESSLRAQVPE 56
 DB 1 MGMTSSMLTYDIEEYVQSHCHDL--FEQOEILSLYQRCQL-----DRNAKGFISAD 50
 QY 57 QILSLPELKANPPEKRICRVFSTSPAKDSLFEDFLDLVSFSDPATPDIKSHYAFRIED 116
 DB 51 EFLSVPEFAMNPLSQRLKLV-----DGLNFKQFVAFLSAFSAKSLRQKQVLIKRYVD 104
 QY 117 FDDDGTLNRDLSRLVNCCLTGEGEDTRLASSEMQLIDNILEEXXXXXXXXQXHV 176
 DB 105 SDGNGKVSFKDIMEVLRLDLSG---SFMSEDEQGVLSQVLEKSGYTSDFLTLEDFIKI 160
 QY 177 ISRS 180
 DB 161 FGSS 164
 RESULT 10
 QBLBK7 PRELIMINARY; PRT; 175 AA.
 AC QBLBK7;
 DT 01-OCT-2002 (TREMblrel. 22, Created)
 DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
 DE Calineurin-like protein.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_Taxid=3702;
 RN RA SEQUENCE FROM N.A.
 RA Haas B.J., Volkovskiy N., Town C.D., Troukhan M., Alexandrov N.,
 RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.,
 RT "Full-length messenger RNA sequences greatly improve genome
 RL annotation.";
 RL Genome Biol. 0:0-0(2002).
 RN RA SEQUENCE FROM N.A.
 RP Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
 RA Feldmann K.,
 RA "Full-length cDNA from Arabidopsis thaliana.";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY087152; AAM64710.1;

DR InterPro: IPR002048; EF-hand.
 DR Pfam: PF00036; efhand; 2.
 DR ProDom: PD000012; EF-hand; 1.
 DR PROSITE: PS00018; EF_HAND; 1.
 SQ SEQUENCE 175 AA; 19932 MW; B26D7E2ADA37AFED CRC64;
 Query Match 20.8%; Score 188; DB 10; Length 175;
 Best Local Similarity 25.0%; Pred. No. 2.8e-07;
 Matches 46; Conservative 57; Mismatches 57; Indels 24; Gaps 5;
 QY 1 MGSGSRSLKELIAEYQ---DLTFLTKQELLAHRRFCELLPQEQRTVESSLRAQVPE 56
 DB 1 MGMTSSMLTYDIEEYVQSHCHDL--FEQOEILSLYQRCQL-----DRNAKGFISAD 50
 QY 57 QILSLPELKANPPEKRICRVFSTSPAKDSLFEDFLDLVSFSDPATPDIKSHYAFRIED 116
 DB 51 EFLSVPEFAMNPLSQRLKLV-----DGLNFKQFVAFLSAFSAKSLRQKQVLIKRYVD 104
 QY 117 FDDDGTLNRDLSRLVNCCLTGEGEDTRLASSEMQLIDNILEEXXXXXXXXQXHV 176
 DB 105 SDGNGKVSFKDIMEVLRLDLSG---SFMSEDEQGVLSQVLEKSGYTSDFLTLEDFIKI 160
 QY 177 ISRS 180
 DB 161 FGSS 164
 RESULT 11
 Q9VNF9 PRELIMINARY; PRT; 189 AA.
 AC Q9VNF9;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-OCT-2002 (TREMblrel. 13, Last sequence update)
 DE CG2185 protein (LD19356p).
 GN CG2185.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_Taxid=7227;
 RN RA SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RX MEDLINE-20196006; PubMed-10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Mitros G.L.G.,
 RA Abail J.F., Adyavani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Bailew R.M., Basu A., Bayendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Burris K.C., Busam D.A., Butler H., Caedieu E., Center A., Chandra I.,
 RA Chertis J.M., Cusum D.A., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos K., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gaborieau A.E., Gary N.S., Galat M.W., Glasser K.,
 RA Glöck A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Mei M.-H., Ibegam C.,
 RA Jalali M., Kalish F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milhina N.V., Mobarry C., Morris J., Moshirefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusslein D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Pui Y., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svrtick R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhao G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Berkeley;
 RA Stapleton M., Brockstein P., Hong L., Appayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA Gonzalez M., Guartin H., Li P., Miao G., Miranda A., Mungall C.J.,
 RA Nuno J., Paecl J., Paragas V., Park S., Pounenavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celinker S.,
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY069465; AAL39610.1;
 DR HSSP: P06705; IAT1;
 DR Flybase: FB9n0037358; CG2185;
 DR InterPro: IPR002048; EF-hand.
 DR Pfam: PF00036; ehand; 2;
 DR Prodom: PD000012; EF-hand; 2;
 DR SMART: SM00054; EFh; 2;
 DR PROSITE: PS00018; EF_HAND; 1;
 DR KEGG: K01101; EF_HAND; 1;
 KW Calcium-binding.
 SQ SEQUENCE 189 AA; 21996 MW; 3621BAF72BED845D CRC64;
 Query Match 19.4%; Score 175.5; DB 5; Length 189;
 Best Local Similarity 23.3%; Pred. No. 3.3e-06;
 Matches 44; Conservative 52; Mismatches 72; Indels 21; Gaps 4;
 QY 1 MGSGGSR-LSKELLAAYODLTLTKOELLARHRCFCELLPOEORTVESSLRAPVEOIL 59
 Db 1 MGKSSLFELRNEETIAQIQEETGFTPNQIERLYSRFTSLDRDCGLSR-----EDLM 52
 QY 60 SLPELANPFEKRICRPFSTSPAKDSLSEDFELLVSF-----SDTPTPIKSHYA 111
 Db 53 RIPELANPFCERIVHSFASNDRVFROFMVNLHFRPLRDNKOSKLSREKLFKA 112
 QY 112 FRIFPDODGTLNREDLSRLVNCITLGEGETRLSASEMKOLIDNILEXXXXXXX 171
 Db 113 FKMVDLDDGIVISDELSTIHMVG-----ANISODQLVSTAERTILEADLCGCKISFE 168
 QY 172 XXQHVISRS 180
 Db 169 DFCRAIDRT 177
 RESULT 12
 Q900X7 PRELIMINARY; PRT; 175 AA.
 AC Q900X7;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Calciaturin subunit.
 GN L7171.06.
 OS Leishmania major.
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=5664;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Friedlin;
 RA Toato V., Bruschi C.V., Ivens A.C., Murphy L., Quail M.,
 RA Rajandream M.A., Barrell B.G.,
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Friedlin;

RX MEDLINE=98146435; PubMed=9477341;
 RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
 RA Smith D.F.,
 RT "A physical map of the *Leishmania major* Friedlin genome.";
 RL Genome Res. 8:135-145(1998).
 DR EMBL: AL133435; CAB62809.1;
 DR HSSP: P06705; IAT1;
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR001125; Recoverin.
 DR Pfam: PF00036; ehand; 4;
 DR PRINTS: PR00450; RECOVERIN.
 DR Prodom: PD000012; EF-hand; 2;
 DR SMART: SM00054; EFh; 3;
 DR PROSITE: PS00018; EF_HAND; 2;
 SQ SEQUENCE 175 AA; 19660 MW; 9448F1274DFA0EB CRC64;
 Query Match 19.2%; Score 174; DB 5; Length 175;
 Best Local Similarity 21.4%; Pred. No. 4e-06;
 Matches 39; Conservative 56; Mismatches 73; Indels 14; Gaps 4;
 QY 8 LSKELLAAYODLTLTKOELLARHRCFCELLPOEORTVESSLRAPVEOILSLPELAN 67
 Db 6 LTAELQNIRESSTALTDQVORLYKFSKLT-----NKOKSGKITRAEFNSIPALASN 57
 QY 68 PFKERICVFTSPAKDSLSEDFELLVSFSDTPTPIKSHYARIFDPPDDGTLNRED 127
 Db 58 PLVPRVLAVMDTD-GDSVTDFGDFRALAVLSATSATSKEDKLFRTFKMYDVDDGRIKMD 116
 QY 128 LSRVNCITLGEGETRLSASEMKOLIDNILEXXXXXXXHXQHVISRSPEFASNF 187
 Db 117 LFGMISTVNG-----VNLSSOMOLOQIVDKTFLEADVDRGIVTFEEFQ-ALAVNSDFGRL 171
 QY 188 KI 189
 Db 172 NL 173
 RESULT 13
 Q8MOT6 PRELIMINARY; PRT; 177 AA.
 AC Q8MOT6;
 DT 01-OCT-2002 (Tremblrel. 22, Created)
 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Protein phosphatase 2B regulatory subunit.
 GN CNB.
 OS Toxoplasma gondii.
 OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;
 OC Toxoplasma.
 OX NCBI_TaxID=5811;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Gaskins E., Kleschick H., Beckers C.J.,
 RT "Identification of the calcineurin A and B subunits of *Toxoplasma gondii*.";
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY125926; AAM97279.1;
 DR InterPro: IPR003299; Calflagin.
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR001125; Recoverin.
 DR Pfam: PF00036; ehand; 4;
 DR PRINTS: PR01362; CALFLAGIN.
 DR PRINTS: PR00450; RECOVERIN.
 DR Prodom: PD000012; EF-hand; 2;
 DR PROSITE: PS00018; EF_HAND; 4;
 SQ SEQUENCE 177 AA; 19994 MW; D588EB0C14F569E8 CRC64;
 Query Match 18.8%; Score 170; DB 5; Length 177;
 Best Local Similarity 21.1%; Pred. No. 8.6e-06;
 Matches 41; Conservative 64; Mismatches 69; Indels 20; Gaps 6;
 QY 1 MGSGGSR-LSKELLAAYODLTLTKOELLARHRCFCELLPOEORTVESSLRAPVEOIL 57
 Db 1 MGKSSLFELRNEETIAQIQEETGFTPNQIERLYSRFTSLDRDCGLSR-----EDLM 52

Db 1 MGNAGRLSPQ---EQMDLHANFSEKDKLYKRF-----RALDTNONGELDTHE 49
 QY 58 ILSPKLANPFRKRICRIVSTSPAKDLSFEDFLDLSVSDTATPDIKSHVAFRIEDF 117
 Db 50 LFDVPELADNPVIRVISTIDTN-GDGKVSFVELVLSKLAANTDFQTKFAPDYDI 108
 QY 118 DDGTLNREDLSRLVNCLTGEGEDTRLASSEMQLIDNILEEXXXXXXXHXOHI 177
 Db 109 NKGSISNGELFAVMKMAVQ-----SNLNDQQLQOLVDRITYQADKDGMSFDFREMV 164
 QY 178 SRSPDFASSPKIYL 191
 Db 165 SHI-DIADKLRLVDL 177

RESULT 14

Q8SRF8 PRELIMINARY; PRT; 200 AA.
 AC Q8SRF8; 01-JUN-2002 (Tremblrel, 21, Created)
 DT 01-JUN-2002 (Tremblrel, 21, Last sequence update)
 DT 01-MAR-2003 (Tremblrel, 23, Last annotation update)
 DE Calchneurin beta subunit.
 GN EC008_0160.
 OS Encephalitozoon cuniculi.
 OC Eukaryota; Fungi; Microsporidia; Unikaryoniidae; Encephalitozoon.
 OX NCBI_Taxid=6035;
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN=GB-M1;
 RA Genoscope;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RN 12
 RP SEQUENCE FROM N.A.
 RC STRAIN=GB-M1;
 RX MEDLINE=21576510; Pubmed=11719806;
 RA Kallina M.D., Duprat S., Cornillot E., Metenier G., Thomarar F.,
 RA Prensier G., Barbe V., Peyretailade E., Brotier P., Wincker P.,
 RA Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
 RA Weissenbach J., Vivares C.P.,
 RT "Genome sequence and gene compaction of the eukaryote parasite
 RT Encephalitozoon cuniculi."
 RL Nature 414:450-453(2001).
 DR EMBL; AL590448; CAD26322.1;
 DR InterPro: IPR002048; EF-hand.
 DR Pfam: PF000036; EF-hand; 3.
 DR SMART: SM00054; EFh; 2.
 SQ SEQUENCE 200 AA; 23929 MW; 3F0A4E2910E87701 CRC64;

Query Match 18.8%; Score 170; DB 5; Length 200;
 Best Local Similarity 23.9%; Pred. No. 1e-05;

Matches 47; Conservative 50; Mismatches 74; Indels 26; Gaps 6;

QY 1 MGS-SGSRLSKELLAEOY-DLFTLKQELILAHRRFCCLLPQEQRTVSSSLRAQVPEOIL 59
 Db 1 MGSLSSTMLCEERIEELKNTYVDEREIEHYERF-QFLDRES-----RGYLTNENL 52
 QY 60 SLPELANPFRKRICRIVSTSPAKDLSFEDFLDLSVSDTATPDIKSHVAFRIEDDD 119
 Db 53 NIPEFSNPFSLIMKSIEMKTDYEMKTEPHLEFLGIFSERNSKRNRIYLFDPIDNG 112
 QY 120 DGTLNREDLSRLVNCLTGEGEDTRLASSEMQLIDNILEEXXXXXXXHXOHI 179
 Db 113 DGLCLNVLIRIKMA---GQDGRVEAE-----NLNLYDEGGKGLDISDFTFYES 163
 QY 180 SP-----DFASSFK 188
 Db 164 DPLIDKNMIDFSKNLK 180

RESULT 15

Q20804 PRELIMINARY; PRT; 171 AA.

AC Q20804;
 DT 01-NOV-1996 (Tremblrel, 01, Created)
 DT 01-MAR-2003 (Tremblrel, 23, Last sequence update)
 DT 01-MAR-2003 (Tremblrel, 23, Last annotation update)
 DE CNB-1 Protein (corresponding sequence F55C10.1).
 GN CNB-1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_Taxid=6239;
 RN 11
 RP SEQUENCE FROM N.A.
 RA Dobson R.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 RN 12
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99069613; Pubmed=9851916;
 RA none;
 RT "Genome sequence of the nematode C. elegans: A platform for
 RT investigating biology."
 RL Science 282:2012-2018(1998).
 DR EMBL; Z74036; CAA98489.3;
 SQ SEQUENCE 171 AA; 19672 MW; 6AB68B3B4A613060 CRC64;

Query Match 18.5%; Score 167.5; DB 5; Length 171;
 Best Local Similarity 24.0%; Pred. No. 1.3e-05;
 Matches 43; Conservative 52; Mismatches 57; Indels 27; Gaps 7;

QY 3 GSGSRLSKELLAEOY-DLFTLKQELILAHRRFCCLLPQEQRTVSSSLRAQVPEOILS 60
 Db 2 GADASLPMEMCSNDAYELRLT-----RRFKL-----DYDGS--GSLVDEPMS 45
 QY 61 LPELANPFRKRICRIVSTSPAKDLSFEDFLDLSVSDTATPDIKSHVAFRIEDDD 120
 Db 46 LPEIQNPVIVQVVIDIFD-EDNGEYDFRERIQISQSVYGDKNLTKLFAFRYIDMDRD 104
 QY 121 GTLNREDLSRLVNCLTGEGEDTRLASSEMQLIDNILEEXXXXXXXHXOHI 175
 Db 105 GFLSNGELFVYLMKMGV-----NMLKDSQLQOIVDKITLHFHDKDGDGRISFQECDDVEH 159

Search completed: July 24, 2003, 13:18:06
 Job time : 98 secs